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(71) Applicant *(for all designated States except US)*: **BAYER AKTIENGESELLSCHAFT** [DE/DE]; 51368 Leverkusen (DE).

(72) Inventor; and
(75) Inventor/Applicant *(for US only)*: **LIOU, Jiing-Ren** [CN/US]; 10 Winslow Road, Belmont, MA 02478 (US).

(74) Common Representative: **BAYER AKTIENGESELLSCHAFT**; 51368 Leverkusen (DE).

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(54) Title: REGULATION OF HUMAN SERINE/THREONINE KINASE

(57) Abstract: Reagents that regulate human serine/threonine kinase and reagents which bind to human serine/threonine kinase gene products can play a role in preventing, ameliorating, or correcting dysfunctions or diseases including, but not limited to, cancer, diabetes, CNS disorders or COPD.

HUMAN SERINE/THREONINE KINASE

This application claims the benefit of and incorporates by reference co-pending provisional application Serial No. 60/318,021 filed August 20, 2001.

TECHNICAL FIELD OF THE INVENTION

The invention relates to the regulation of human serine/threonine kinase.

BACKGROUND OF THE INVENTION

Intercellular signaling regulates a variety of important biological functions. For example, transforming growth factor type beta (TGF-β) regulates the proliferation and differentiation of a variety of cell types binding to and activating cell surface receptors which possess serine-threonine kinase activity. Atfi *et al.* (*Proc. Natl. Acad. Sci. U.S.A. 92,* 12110-04, 1995) have shown that TGF-β activates a 78-kDa protein (p78) serine/threonine kinase; the p78 kinase was activated only in cells for which TGF-β acts as a growth inhibitory factor. Because of the important functions of kinases such as p78, there is a need in the art to identify new kinases and methods of regulating these new kinases for therapeutic effects.

SUMMARY OF THE INVENTION

It is an object of the invention to provide reagents and methods of regulating a human serine/threonine kinase. This and other objects of the invention are provided by one or more of the embodiments described below.

One embodiment of the invention is a serine/threonine kinase polypeptide comprising an amino acid sequence selected from the group consisting of:

amino acid sequences which are at least about 30% identical to the amino acid sequence shown in SEQ ID NO: 2;

the amino acid sequence shown in SEQ ID NO: 2;

amino acid sequences which are at least about 30% identical to the amino acid sequence shown in SEQ ID NO: 5; and

the amino acid sequence shown in SEQ ID NO: 5.

Yet another embodiment of the invention is a method of screening for agents which decrease extracellular matrix degradation. A test compound is contacted with a serine/threonine kinase polypeptide comprising an amino acid sequence selected from the group consisting of:

amino acid sequences which are at least about 30% identical to the amino acid sequence shown in SEQ ID NO: 2;

the amino acid sequence shown in SEQ ID NO: 2;

amino acid sequences which are at least about 30% identical to the amino acid sequence shown in SEQ ID NO: 5; and

the amino acid sequence shown in SEQ ID NO: 5.

Binding between the test compound and the serine/threonine kinase polypeptide is detected. A test compound which binds to the serine/threonine kinase polypeptide is thereby identified as a potential agent for decreasing extracellular matrix degradation. The agent can work by decreasing the activity of the serine/threonine kinase.

Another embodiment of the invention is a method of screening for agents which decrease extracellular matrix degradation. A test compound is contacted with a polynucleotide encoding a serine/threonine kinase polypeptide, wherein the polynucleotide comprises a nucleotide sequence selected from the group consisting of:

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 1;

the nucleotide sequence shown in SEQ ID NO: 1;

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 4;

the nucleotide sequence shown in SEQ ID NO: 4;

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 8; and

the nucleotide sequence shown in SEQ ID NO:8.

Binding of the test compound to the polynucleotide is detected. A test compound which binds to the polynucleotide is identified as a potential agent for decreasing extracellular matrix degradation. The agent can work by decreasing the amount of the serine/threonine kinase through interacting with the serine/threonine kinase mRNA.

Another embodiment of the invention is a method of screening for agents which regulate extracellular matrix degradation. A test compound is contacted with a serine/threonine kinase polypeptide comprising an amino acid sequence selected from the group consisting of:

amino acid sequences which are at least about 30% identical to the amino acid sequence shown in SEQ ID NO: 2;

the amino acid sequence shown in SEQ ID NO: 2;

amino acid sequences which are at least about 30% identical to the amino acid sequence shown in SEQ ID NO: 5; and

the amino acid sequence shown in SEQ ID NO: 5.

A serine/threonine kinase activity of the polypeptide is detected. A test compound which increases serine/threonine kinase activity of the polypeptide relative to serine/threonine kinase activity in the absence of the test compound is thereby identified as a potential agent for increasing extracellular matrix degradation. A test compound which decreases serine/threonine kinase activity of the polypeptide relative to serine/threonine kinase activity in the absence of the test compound is thereby identified as a potential agent for decreasing extracellular matrix degradation.

Even another embodiment of the invention is a method of screening for agents which decrease extracellular matrix degradation. A test compound is contacted with a serine/threonine kinase product of a polynucleotide which comprises a nucleotide sequence selected from the group consisting of:

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 1;

the nucleotide sequence shown in SEQ ID NO: 1;

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 4;

the nucleotide sequence shown in SEQ ID NO: 4;

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 8; and

the nucleotide sequence shown in SEQ ID NO:8.

Binding of the test compound to the serine/threonine kinase product is detected. A test compound which binds to the serine/threonine kinase product is thereby identified as a potential agent for decreasing extracellular matrix degradation.

Still another embodiment of the invention is a method of reducing extracellular matrix degradation. A cell is contacted with a reagent which specifically binds to a polynucleotide encoding a serine/threonine kinase polypeptide or the product encoded by the polynucleotide, wherein the polynucleotide comprises a nucleotide sequence selected from the group consisting of:

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 1;

the nucleotide sequence shown in SEQ ID NO: 1;

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 4;

the nucleotide sequence shown in SEQ ID NO: 4;

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 8; and

the nucleotide sequence shown in SEQ ID NO: 8.

Serine/threonine kinase activity in the cell is thereby decreased.

The invention thus provides a human serine/threonine kinase that can be used to identify test compounds that may act, for example, as activators or inhibitors at the enzyme's active site. Human serine/threonine kinase and fragments thereof also are useful in raising specific antibodies that can block the enzyme and effectively reduce its activity.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows the DNA-sequence encoding a serine/threonine kinase polypeptide (SEQ ID NO:1).

Fig. 2 shows the amino acid sequence deduced from the DNA-sequence of Fig.1 (SEQ ID NO:2).

Fig. 3 shows the amino acid sequence of the protein identified by swiss|P41243|MATK_RAT (SEQ ID NO:3).

Fig. 4 shows the DNA-sequence encoding a serine/threonine kinase polypeptide (SEQ ID NO:4).

Fig. 5 shows the amino acid sequence deduced from the DNA-sequence of Fig. 4 (SEQ ID NO:5).

Fig. 6 shows the amino acid sequence of the protein identified by trembl|Z48615|HSMSTMR_1 (SEQ ID NO:6).

Fig. 7 shows the amino acid sequence of the protein identified by tremblnew|AK014886|AK014886_1 (SEQ ID NO: 7).

Fig. 8 shows the DNA-sequence encoding a serine/threonine kinase Polypeptide (SEQ ID NO:8).

Fig. 9 shows the BLASTP - alignment of 495 (SEQ ID NO:2) against swiss|P41243|MATK_RAT (SEQ ID NO:3).

Fig. 10 shows the BLASTP - alignment of 495 (SEQ ID NO:2) against trembl|Z48615|HSMSTMR_1 (SEQ ID NO:6).

Fig. 11 shows the BLASTP - alignment of 495 (SEQ ID NO:2) against swissnew|P80192|M3K9_HUMAN (SEQ ID NO:7).

Fig. 12 shows the BLASTP - alignment of 495 (SEQ ID NO:2) against tremblnew|AK014886|AK014886_1 (SEQ ID NO:7).

Fig. 13 shows the 3D structure: BLASTP - alignment of 495 (SEQ ID NO:2) against pdb|1AGW|1AGW-B.

Fig. 14 shows the HMMPFAM - alignment of 495 (SEQ ID NO:2) against pfam|hmm|pkinase.

Fig. 15 shows the BLASTP - alignment of 495_Protein (SEQ ID NO:5) against trembl|AK014886|AK014886_1 (SEQ ID NO:6).

Fig. 16 shows the exon-intron structure prediction by Genewise.

Fig. 17 shows the relative mRNA expression of the novel serine/threonine kinase in human tissues.

Fig. 18 shows the relative mRNA expression of the novel serine/threonine kinase in human cells and tissues that are implicated in chronic lung disease such as COPD.

DETAILED DESCRIPTION OF THE INVENTION

The invention relates to an isolated polynucleotide from the group consisting of:

a) a polynucleotide encoding a serine/threonine kinase polypeptide comprising an amino acid sequence selected from the group consisting of:
amino acid sequences which are at least about 30% identical to the amino acid sequence shown in SEQ ID NO: 2;
the amino acid sequence shown in SEQ ID NO: 2;
amino acid sequences which are at least about 30% identical to the amino acid sequence shown in SEQ ID NO: 5; and
the amino acid sequence shown in SEQ ID NO:5.

b) a polynucleotide comprising the sequence of SEQ ID NOS: 1, 4 or 8;

c) a polynucleotide which hybridizes under stringent conditions to a polynucleotide specified in (a) and (b) and encodes a serine/threonine kinase polypeptide;

d) a polynucleotide the sequence of which deviates from the polynucleotide sequences specified in (a) to (c) due to the degeneration of the genetic code and encodes a serine/threonine kinase polypeptide; and

e) a polynucleotide which represents a fragment, derivative or allelic variation of a polynucleotide sequence specified in (a) to (d) and encodes a serine/threonine kinase polypeptide.

Furthermore, it has been discovered by the present applicant that a novel serine/threonine kinase, particularly a human serine/threonine kinase, can be used in therapeutic methods to treat cancer, diabetes, CNS disorders or COPD. Human serine/threonine kinase comprises the amino acid sequence shown in SEQ ID NO:2 or 5. Coding sequences are shown in SEQ ID NO:1 and 4, respectively. These sequence is located on chromosome 12. Related ESTs (AF114068; BE177830; BE178563; BE175531; BE175603; BE175601; embl|AV705213|AV705213; embl|BE177830|BE177830; embl|BE175531|BE175531; embl|BE175603|BE175603; embl|BE175601|BE175601; embl|AA278893|AA278893; embl|BG189993|BG189993; embl|BF351566|BF351566; embl|BG546973|BG546973) are expressed in head_neck and kidney, as well as in adrenal gland, germinal center B cells, and lung. Alignments are shown in FIGS. 9-16.

Human serine/threonine kinase is 29% identical over 259 amino acids to serine/threonine kinase (FIG. 1).

Human serine/threonine kinase of the invention is expected to be useful for the same purposes as previously identified serine/threonine kinase enzymes. Human serine/threonine kinase is believed to be useful in therapeutic methods to treat disorders such as cancer, diabetes, CNS disorders, and COPD. Human serine/threonine

kinase also can be used to screen for human serine/threonine kinase activators and inhibitors.

Polypeptides

Human serine/threonine kinase polypeptides according to the invention comprise at least 6, 10, 15, 20, 25, 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, or 592 contiguous amino acids selected from the amino acid sequence shown in SEQ ID NO:2 or at least 6, 10, 15, 20, 25, 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600, 700, 800, 900, or 983 contiguous amino acids selected from the amino acid sequence shown in SEQ ID NO:5 or a biologically active variant thereof, as defined below. A serine/threonine kinase polypeptide of the invention therefore can be a portion of a serine/threonine kinase, a full-length serine/threonine kinase, or a fusion protein comprising all or a portion of a serine/threonine kinase.

Biologically Active Variants

serine/threonine kinase polypeptide variants that are biologically active, *i.e.*, retain the ability to bind a ligand to produce a biological effect, such as cyclic AMP formation, mobilization of intracellular calcium, or phosphoinositide metabolism, also are serine/threonine kinase polypeptides. Preferably, naturally or non-naturally occurring serine/threonine kinase polypeptide variants have amino acid sequences which are at least about 30, preferably at least about 35, 55, 65, 70, 75, 90, 96, or 98% identical to the amino acid sequence shown in SEQ ID NO:2 or 5 a fragment thereof. Percent identity between a putative serine/threonine kinase polypeptide variant and an amino acid sequence of SEQ ID NO:2 or 5 is determined by conventional methods. See, for example, Altschul *et al.*, *Bull. Math. Bio. 48*:603 (1986), and Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA 89*:10915 (1992). Briefly, two amino acid sequences are aligned to optimize the alignment scores using a gap opening penalty of 10, a gap extension penalty of 1, and the "BLOSUM62"

scoring matrix of Henikoff & Henikoff, 1992.

Those skilled in the art appreciate that there are many established algorithms available to align two amino acid sequences. The "FASTA" similarity search algorithm of Pearson & Lipman is a suitable protein alignment method for examining the level of identity shared by an amino acid sequence disclosed herein and the amino acid sequence of a putative variant. The FASTA algorithm is described by Pearson & Lipman, *Proc. Nat'l Acad. Sci. USA 85*:2444(1988), and by Pearson, *Meth. Enzymol. 183*:63 (1990). Briefly, FASTA first characterizes sequence similarity by identifying regions shared by the query sequence (*e.g.*, SEQ ID NO: 2 or 5) and a test sequence that have either the highest density of identities (if the ktup variable is 1) or pairs of identities (if ktup=2), without considering conservative amino acid substitutions, insertions, or deletions. The ten regions with the highest density of identities are then rescored by comparing the similarity of all paired amino acids using an amino acid substitution matrix, and the ends of the regions are "trimmed" to include only those residues that contribute to the highest score. If there are several regions with scores greater than the "cutoff" value (calculated by a predetermined formula based upon the length of the sequence the ktup value), then the trimmed initial regions are examined to determine whether the regions can be joined to form an approximate alignment with gaps. Finally, the highest scoring regions of the two amino acid sequences are aligned using a modification of the Needleman-Wunsch- Sellers algorithm (Needleman & Wunsch, *J. Mol. Biol.48*:444 (1970); Sellers, *SIAM J. Appl. Math.26*:787 (1974)), which allows for amino acid insertions and deletions. Preferred parameters for FASTA analysis are: ktup=1, gap opening penalty=10, gap extension penalty=1, and substitution matrix=BLOSUM62. These parameters can be introduced into a FASTA program by modifying the scoring matrix file ("SMATRIX"), as explained in Appendix 2 of Pearson, *Meth. Enzymol. 183*:63 (1990).

FASTA can also be used to determine the sequence identity of nucleic acid molecules using a ratio as disclosed above. For nucleotide sequence comparisons,

the ktup value can range between one to six, preferably from three to six, most preferably three, with other parameters set as default.

Variations in percent identity can be due, for example, to amino acid substitutions, insertions, or deletions. Amino acid substitutions are defined as one for one amino acid replacements. They are conservative in nature when the substituted amino acid has similar structural and/or chemical properties. Examples of conservative replacements are substitution of a leucine with an isoleucine or valine, an aspartate with a glutamate, or a threonine with a serine.

Amino acid insertions or deletions are changes to or within an amino acid sequence. They typically fall in the range of about 1 to 5 amino acids. Guidance in determining which amino acid residues can be substituted, inserted, or deleted without abolishing biological or immunological activity of a serine/threonine kinase polypeptide can be found using computer programs well known in the art, such as DNASTAR software.

The invention additionally, encompasses serine/threonine kinase polypeptides that are differentially modified during or after translation, *e.g.*, by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications can be carried out by known techniques including, but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, $NaBH_4$, acetylation, formylation, oxidation, reduction, metabolic synthesis in the presence of tunicamycin, etc.

Additional post-translational modifications encompassed by the invention include, for example, *e.g.*, N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends), attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of prokaryotic

host cell expression. The serine/threonine kinase polypeptides may also be modified with a detectable label, such as an enzymatic, fluorescent, isotopic or affinity label to allow for detection and isolation of the protein.

The invention also provides chemically modified derivatives of serine/threonine kinase polypeptides that may provide additional advantages such as increased solubility, stability and circulating time of the polypeptide, or decreased immunogenicity (see U.S. Patent No. 4,179,337). The chemical moieties for derivitization can be selected from water soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol, and the like. The polypeptides can be modified at random or predetermined positions within the molecule and can include one, two, three, or more attached chemical moieties.

Whether an amino acid change or a polypeptide modification results in a biologically active serine/threonine kinase polypeptide can readily be determined by assaying for binding to a ligand or by conducting a functional assay, as described for example, in Trost *et al.*, *J. Biol. Chem. 275*, 7373-77, 2000; Hayashi *et al.*, *Biochem. Biophys. Res. Commun. 264*, 449-56, 1999; Masure *et al.*, *Eur. J. Biochem. 265*, 353-60, 1999; and Mukhopadhyay *et al.*, *J. Bacteriol. 181*, 6615-22, 1999.

Fusion Proteins

Fusion proteins are useful for generating antibodies against serine/threonine kinase polypeptide amino acid sequences and for use in various assay systems. For example, fusion proteins can be used to identify proteins that interact with portions of a serine/threonine kinase polypeptide. Protein affinity chromatography or library-based assays for protein-protein interactions, such as the yeast two-hybrid or phage display systems, can be used for this purpose. Such methods are well known in the art and also can be used as drug screens.

A serine/threonine kinase polypeptide fusion protein comprises two polypeptide segments fused together by means of a peptide bond. The first polypeptide segment comprises at least 6, 10, 15, 20, 25, 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, or 592 contiguous amino acids selected from the amino acid sequence shown in SEQ ID NO:2 or at least 6, 10, 15, 20, 25, 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600, 700, 800, 900, or 983 or of a biologically active variant, such as those described above. The first polypeptide segment also can comprise full-length serine/threonine kinase.

The second polypeptide segment can be a full-length protein or a protein fragment. Proteins commonly used in fusion protein construction include β-galactosidase, β-glucuronidase, green fluorescent protein (GFP), autofluorescent proteins, including blue fluorescent protein (BFP), glutathione-S-transferase (GST), luciferase, horse-radish peroxidase (HRP), and chloramphenicol acetyltransferase (CAT). Additionally, epitope tags are used in fusion protein constructions, including histidine (His) tags, FLAG tags, influenza hemagglutinin (HA) tags, Myc tags, VSV-G tags, and thioredoxin (Trx) tags. Other fusion constructions can include maltose binding protein (MBP), S-tag, Lex a DNA binding domain (DBD) fusions, GAL4 DNA binding domain fusions, and herpes simplex virus (HSV) BP16 protein fusions.

A fusion protein also can be engineered to contain a cleavage site located between the serine/threonine kinase polypeptide-encoding sequence and the heterologous protein sequence, so that the serine/threonine kinase polypeptide can be cleaved and purified away from the heterologous moiety.

A fusion protein can be synthesized chemically, as is known in the art. Preferably, a fusion protein is produced by covalently linking two polypeptide segments or by standard procedures in the art of molecular biology. Recombinant DNA methods can be used to prepare fusion proteins, for example, by making a DNA construct which comprises coding sequences selected from SEQ ID NO:1 or 10 in proper reading frame with nucleotides encoding the second polypeptide segment and

expressing the DNA construct in a host cell, as is known in the art. Many kits for constructing fusion proteins are available from companies such as Promega Corporation (Madison, WI), Stratagene (La Jolla, CA), CLONTECH (Mountain View, CA), Santa Cruz Biotechnology (Santa Cruz, CA), MBL International Corporation (MIC; Watertown, MA), and Quantum Biotechnologies (Montreal, Canada; 1-888-DNA-KITS).

Identification of Species Homologs

Species homologs of human serine/threonine kinase polypeptide can be obtained using serine/threonine kinase polypeptide polynucleotides (described below) to make suitable probes or primers for screening cDNA expression libraries from other species, such as mice, monkeys, or yeast, identifying cDNAs which encode homologs of serine/threonine kinase polypeptide, and expressing the cDNAs as is known in the art.

Polynucleotides

A serine/threonine kinase polynucleotide can be single- or double-stranded and comprises a coding sequence or the complement of a coding sequence for a serine/threonine kinase polypeptide. Coding sequences for human serine/threonine kinase are shown in SEQ ID NO:1 and 4.

Degenerate nucleotide sequences encoding human serine/threonine kinase polypeptides, as well as homologous nucleotide sequences which are at least about 50, 55, 60, 65, 70, preferably about 75, 90, 96, 98, or 99% identical to the nucleotide sequence shown in SEQ ID NO:1 or 4 or its complement also are serine/threonine kinase polynucleotides. Percent sequence identity between the sequences of two polynucleotides is determined using computer programs such as ALIGN which employ the FASTA algorithm, using an affine gap search with a gap open penalty of -12 and a gap extension penalty of -2. Complementary DNA (cDNA) molecules,

species homologs, and variants of serine/threonine kinase polynucleotides that encode biologically active serine/threonine kinase polypeptides also are serine/threonine kinase polynucleotides. Polynucleotide fragments comprising at least 8, 9, 10, 11, 12, 15, 20, or 25 contiguous nucleotides of SEQ ID NO:1 or 4 or its complement also are serine/threonine kinase polynucleotides. These fragments can be used, for example, as hybridization probes or as antisense oligonucleotides.

Identification of Polynucleotide Variants and Homologs

Variants and homologs of the serine/threonine kinase polynucleotides described above also are serine/threonine kinase polynucleotides. Typically, homologous serine/threonine kinase polynucleotide sequences can be identified by hybridization of candidate polynucleotides to known serine/threonine kinase polynucleotides under stringent conditions, as is known in the art. For example, using the following wash conditions--2X SSC (0.3 M NaCl, 0.03 M sodium citrate, pH 7.0), 0.1% SDS, room temperature twice, 30 minutes each; then 2X SSC, 0.1% SDS, 50 °C once, 30 minutes; then 2X SSC, room temperature twice, 10 minutes each--homologous sequences can be identified which contain at most about 25-30% basepair mismatches. More preferably, homologous nucleic acid strands contain 15-25% basepair mismatches, even more preferably 5-15% basepair mismatches.

Species homologs of the serine/threonine kinase polynucleotides disclosed herein also can be identified by making suitable probes or primers and screening cDNA expression libraries from other species, such as mice, monkeys, or yeast. Human variants of serine/threonine kinase polynucleotides can be identified, for example, by screening human cDNA expression libraries. It is well known that the T_m of a double-stranded DNA decreases by 1-1.5 °C with every 1% decrease in homology (Bonner *et al.*, *J. Mol. Biol. 81*, 123 (1973). Variants of human serine/threonine kinase polynucleotides or serine/threonine kinase polynucleotides of other species can therefore be identified by hybridizing a putative homologous serine/threonine kinase polynucleotide with a polynucleotide having a nucleotide sequence of SEQ ID

NO:1 or 4 or the complement thereof to form a test hybrid. The melting temperature of the test hybrid is compared with the melting temperature of a hybrid comprising polynucleotides having perfectly complementary nucleotide sequences, and the number or percent of basepair mismatches within the test hybrid is calculated.

Nucleotide sequences which hybridize to serine/threonine kinase polynucleotides or their complements following stringent hybridization and/or wash conditions also are serine/threonine kinase polynucleotides. Stringent wash conditions are well known and understood in the art and are disclosed, for example, in Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL, 2d ed., 1989, at pages 9.50-9.51.

Typically, for stringent hybridization conditions a combination of temperature and salt concentration should be chosen that is approximately 12-20 °C below the calculated T_m of the hybrid under study. The T_m of a hybrid between a serine/threonine kinase polynucleotide having a nucleotide sequence shown in SEQ ID NO:1 or the complement thereof and a polynucleotide sequence which is at least about 50, preferably about 75, 90, 96, or 98% identical to one of those nucleotide sequences can be calculated, for example, using the equation of Bolton and McCarthy, *Proc. Natl. Acad. Sci. U.S.A. 48*, 1390 (1962):

$$T_m = 81.5\ ^{\circ}C - 16.6(\log_{10}[Na^+]) + 0.41(\%G + C) - 0.63(\%formamide) - 600/l),$$

where l = the length of the hybrid in basepairs.

Stringent wash conditions include, for example, 4X SSC at 65 °C, or 50% formamide, 4X SSC at 42 °C, or 0.5X SSC, 0.1% SDS at 65 °C. Highly stringent wash conditions include, for example, 0.2X SSC at 65 °C.

Preparation of Polynucleotides

A serine/threonine kinase polynucleotide can be isolated free of other cellular components such as membrane components, proteins, and lipids. Polynucleotides

can be made by a cell and isolated using standard nucleic acid purification techniques, or synthesized using an amplification technique, such as the polymerase chain reaction (PCR), or by using an automatic synthesizer. Methods for isolating polynucleotides are routine and are known in the art. Any such technique for obtaining a polynucleotide can be used to obtain isolated serine/threonine kinase polynucleotides. For example, restriction enzymes and probes can be used to isolate polynucleotide fragments, which comprise serine/threonine kinase nucleotide sequences. Isolated polynucleotides are in preparations that are free or at least 70, 80, or 90% free of other molecules.

Human serine/threonine kinase cDNA molecules can be made with standard molecular biology techniques, using serine/threonine kinase mRNA as a template. Human serine/threonine kinase cDNA molecules can thereafter be replicated using molecular biology techniques known in the art and disclosed in manuals such as Sambrook *et al.* (1989). An amplification technique, such as PCR, can be used to obtain additional copies of polynucleotides of the invention, using either human genomic DNA or cDNA as a template.

Alternatively, synthetic chemistry techniques can be used to synthesize serine/threonine kinase polynucleotides. The degeneracy of the genetic code allows alternate nucleotide sequences to be synthesized which will encode a serine/threonine kinase polypeptide having, for example, an amino acid sequence shown in SEQ ID NO:2 or a biologically active variant thereof.

Extending Polynucleotides

Various PCR-based methods can be used to extend the nucleic acid sequences disclosed herein to detect upstream sequences such as promoters and regulatory elements. For example, restriction-site PCR uses universal primers to retrieve unknown sequence adjacent to a known locus (Sarkar, *PCR Methods Applic. 2*, 318-322, 1993). Genomic DNA is first amplified in the presence of a primer to a

linker sequence and a primer specific to the known region. The amplified sequences are then subjected to a second round of PCR with the same linker primer and another specific primer internal to the first one. Products of each round of PCR are transcribed with an appropriate RNA polymerase and sequenced using reverse transcriptase.

Inverse PCR also can be used to amplify or extend sequences using divergent primers based on a known region (Triglia *et al.*, *Nucleic Acids Res. 16*, 8186, 1988). Primers can be designed using commercially available software, such as OLIGO 4.06 Primer Analysis software (National Biosciences Inc., Plymouth, Minn.), to be 22-30 nucleotides in length, to have a GC content of 50% or more, and to anneal to the target sequence at temperatures about 68-72 °C. The method uses several restriction enzymes to generate a suitable fragment in the known region of a gene. The fragment is then circularized by intramolecular ligation and used as a PCR template.

Another method which can be used is capture PCR, which involves PCR amplification of DNA fragments adjacent to a known sequence in human and yeast artificial chromosome DNA (Lagerstrom *et al.*, *PCR Methods Applic. 1*, 111-119, 1991). In this method, multiple restriction enzyme digestions and ligations also can be used to place an engineered double-stranded sequence into an unknown fragment of the DNA molecule before performing PCR.

Another method which can be used to retrieve unknown sequences is that of Parker *et al.*, *Nucleic Acids Res. 19*, 3055-3060, 1991). Additionally, PCR, nested primers, and PROMOTERFINDER libraries (CLONTECH, Palo Alto, Calif.) can be used to walk genomic DNA (CLONTECH, Palo Alto, Calif.). This process avoids the need to screen libraries and is useful in finding intron/exon junctions.

When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. Randomly-primed libraries are preferable, in that they will contain more sequences which contain the 5' regions of genes. Use of

a randomly primed library may be especially preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries can be useful for extension of sequence into 5' non-transcribed regulatory regions.

Commercially available capillary electrophoresis systems can be used to analyze the size or confirm the nucleotide sequence of PCR or sequencing products. For example, capillary sequencing can employ flowable polymers for electrophoretic separation, four different fluorescent dyes (one for each nucleotide) that are laser activated, and detection of the emitted wavelengths by a charge coupled device camera. Output/light intensity can be converted to electrical signal using appropriate software (*e.g.* GENOTYPER and Sequence NAVIGATOR, Perkin Elmer), and the entire process from loading of samples to computer analysis and electronic data display can be computer controlled. Capillary electrophoresis is especially preferable for the sequencing of small pieces of DNA that might be present in limited amounts in a particular sample.

Obtaining Polypeptides

Human serine/threonine kinase polypeptides can be obtained, for example, by purification from human cells, by expression of serine/threonine kinase polynucleotides, or by direct chemical synthesis.

Protein Purification

Human serine/threonine kinase polypeptides can be purified from any cell that expresses the polypeptide, including host cells that have been transfected with serine/threonine kinase expression constructs. A purified serine/threonine kinase polypeptide is separated from other compounds that normally associate with the serine/threonine kinase polypeptide in the cell, such as certain proteins, carbohydrates, or lipids, using methods well-known in the art. Such methods include, but are not limited to, size exclusion chromatography, ammonium sulfate fractionation,

ion exchange chromatography, affinity chromatography, and preparative gel electrophoresis. A preparation of purified serine/threonine kinase polypeptides is at least 80% pure; preferably, the preparations are 90%, 95%, or 99% pure. Purity of the preparations can be assessed by any means known in the art, such as SDS-polyacrylamide gel electrophoresis.

Expression of Polynucleotides

To express a serine/threonine kinase polynucleotide, the polynucleotide can be inserted into an expression vector that contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods that are well known to those skilled in the art can be used to construct expression vectors containing sequences encoding serine/threonine kinase polypeptides and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. Such techniques are described, for example, in Sambrook *et al.* (1989) and in Ausubel *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, N.Y., 1989.

A variety of expression vector/host systems can be utilized to contain and express sequences encoding a serine/threonine kinase polypeptide. These include, but are not limited to, microorganisms, such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors, insect cell systems infected with virus expression vectors (*e.g.*, baculovirus), plant cell systems transformed with virus expression vectors (*e.g.*, cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (*e.g.*, Ti or pBR322 plasmids), or animal cell systems.

The control elements or regulatory sequences are those non-translated regions of the vector -- enhancers, promoters, 5' and 3' untranslated regions -- which interact with host cellular proteins to carry out transcription and translation. Such elements can

vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, can be used. For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the BLUESCRIPT phagemid (Stratagene, LaJolla, Calif.) or pSPORT1 plasmid (Life Technologies) and the like can be used. The baculovirus polyhedrin promoter can be used in insect cells. Promoters or enhancers derived from the genomes of plant cells (*e.g.*, heat shock, RUBISCO, and storage protein genes) or from plant viruses (*e.g.*, viral promoters or leader sequences) can be cloned into the vector. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses are preferable. If it is necessary to generate a cell line that contains multiple copies of a nucleotide sequence encoding a serine/threonine kinase polypeptide, vectors based on SV40 or EBV can be used with an appropriate selectable marker.

Bacterial and Yeast Expression Systems

In bacterial systems, a number of expression vectors can be selected depending upon the use intended for the serine/threonine kinase polypeptide. For example, when a large quantity of a serine/threonine kinase polypeptide is needed for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified can be used. Such vectors include, but are not limited to, multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene). In a BLUESCRIPT vector, a sequence encoding the serine/threonine kinase polypeptide can be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of β-galactosidase so that a hybrid protein is produced. pIN vectors (Van Heeke & Schuster, *J. Biol. Chem. 264*, 5503-5509, 1989) or pGEX vectors (Promega, Madison, Wis.) also can be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems can be designed to include

heparin, thrombin, or factor Xa protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

In the yeast *Saccharomyces cerevisiae*, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH can be used. For reviews, see Ausubel *et al.* (1989) and Grant *et al.*, *Methods Enzymol. 153*, 516-544, 1987.

Plant and Insect Expression Systems

If plant expression vectors are used, the expression of sequences encoding serine/threonine kinase polypeptides can be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of CaMV can be used alone or in combination with the omega leader sequence from TMV (Takamatsu, *EMBO J. 6*, 307-311, 1987). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters can be used (Coruzzi *et al.*, *EMBO J. 3*, 1671-1680, 1984; Broglie *et al.*, *Science 224*, 838-843, 1984; Winter *et al.*, *Results Probl. Cell Differ. 17*, 85-105, 1991). These constructs can be introduced into plant cells by direct DNA transformation or by pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (*e.g.*, Hobbs or Murray, in McGraw Hill Yearbook of Science and Technology, McGraw Hill, New York, N.Y., pp. 191-196, 1992).

An insect system also can be used to express a serine/threonine kinase polypeptide. For example, in one such system *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia* larvae. Sequences encoding serine/threonine kinase polypeptides can be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of serine/threonine kinase polypeptides will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses can then

be used to infect *S. frugiperda cells* or *Trichoplusia* larvae in which serine/threonine kinase polypeptides can be expressed (Engelhard *et al.*, *Proc. Nat. Acad. Sci. 91*, 3224-3227, 1994).

Mammalian Expression Systems

A number of viral-based expression systems can be used to express serine/threonine kinase polypeptides in mammalian host cells. For example, if an adenovirus is used as an expression vector, sequences encoding serine/threonine kinase polypeptides can be ligated into an adenovirus transcription/translation complex comprising the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome can be used to obtain a viable virus that is capable of expressing a serine/threonine kinase polypeptide in infected host cells (Logan & Shenk, *Proc. Natl. Acad. Sci. 81*, 3655-3659, 1984). If desired, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, can be used to increase expression in mammalian host cells.

Human artificial chromosomes (HACs) also can be used to deliver larger fragments of DNA than can be contained and expressed in a plasmid. HACs of 6M to 10M are constructed and delivered to cells via conventional delivery methods (*e.g.*, liposomes, polycationic amino polymers, or vesicles).

Specific initiation signals also can be used to achieve more efficient translation of sequences encoding serine/threonine kinase polypeptides. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding a serine/threonine kinase polypeptide, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals (including the ATG initiation codon) should be provided. The initiation codon should be in the correct reading frame to ensure translation of the entire insert.

Exogenous translational elements and initiation codons can be of various origins, both natural and synthetic. The efficiency of expression can be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used (see Scharf *et al.*, *Results Probl. Cell Differ. 20*, 125-162, 1994).

Host Cells

A host cell strain can be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed serine/threonine kinase polypeptide in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the polypeptide also can be used to facilitate correct insertion, folding and/or function. Different host cells that have specific cellular machinery and characteristic mechanisms for post-translational activities (*e.g.*, CHO, HeLa, MDCK, HEK293, and WI38), are available from the American Type Culture Collection (ATCC; 10801 University Boulevard, Manassas, VA 20110-2209) and can be chosen to ensure the correct modification and processing of the foreign protein.

Stable expression is preferred for long-term, high-yield production of recombinant proteins. For example, cell lines which stably express serine/threonine kinase polypeptides can be transformed using expression vectors which can contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells can be allowed to grow for 1-2 days in an enriched medium before they are switched to a selective medium. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced serine/threonine kinase sequences. Resistant clones of stably transformed cells can be proliferated using tissue culture techniques appropriate to the cell type. See, for example, ANIMAL CELL CULTURE, R.I. Freshney, ed., 1986.

Any number of selection systems can be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler *et al.*, *Cell 11*, 223-32, 1977) and adenine phosphoribosyltransferase (Lowy *et al.*, *Cell 22*, 817-23, 1980) genes which can be employed in *tk*⁻ or *aprt*⁻ cells, respectively. Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate (Wigler *et al.*, *Proc. Natl. Acad. Sci. 77*, 3567-70, 1980), *npt* confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin *et al.*, *J. Mol. Biol. 150*, 1-14, 1981), and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murray, 1992, *supra*). Additional selectable genes have been described. For example, *trpB* allows cells to utilize indole in place of tryptophan, or *hisD*, which allows cells to utilize histinol in place of histidine (Hartman & Mulligan, *Proc. Natl. Acad. Sci. 85*, 8047-51, 1988). Visible markers such as anthocyanins, β-glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, can be used to identify transformants and to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes *et al.*, *Methods Mol. Biol. 55*, 121-131, 1995).

<u>*Detecting Expression*</u>

Although the presence of marker gene expression suggests that the serine/threonine kinase polynucleotide is also present, its presence and expression may need to be confirmed. For example, if a sequence encoding a serine/threonine kinase polypeptide is inserted within a marker gene sequence, transformed cells containing sequences that encode a serine/threonine kinase polypeptide can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding a serine/threonine kinase polypeptide under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the serine/threonine kinase polynucleotide.

Alternatively, host cells which contain a serine/threonine kinase polynucleotide and which express a serine/threonine kinase polypeptide can be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay or immunoassay techniques that include membrane, solution, or chip-based technologies for the detection and/or quantification of nucleic acid or protein. For example, the presence of a polynucleotide sequence encoding a serine/threonine kinase polypeptide can be detected by DNA-DNA or DNA-RNA hybridization or amplification using probes or fragments or fragments of polynucleotides encoding a serine/threonine kinase polypeptide. Nucleic acid amplification-based assays involve the use of oligonucleotides selected from sequences encoding a serine/threonine kinase polypeptide to detect transformants that contain a serine/threonine kinase polynucleotide.

A variety of protocols for detecting and measuring the expression of a serine/threonine kinase polypeptide, using either polyclonal or monoclonal antibodies specific for the polypeptide, are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immuno-assay using monoclonal antibodies reactive to two non-interfering epitopes on a serine/threonine kinase polypeptide can be used, or a competitive binding assay can be employed. These and other assays are described in Hampton *et al.*, SEROLOGICAL METHODS: A LABORATORY MANUAL, APS Press, St. Paul, Minn., 1990) and Maddox *et al.*, *J. Exp. Med. 158*, 1211-1216, 1983).

A wide variety of labels and conjugation techniques are known by those skilled in the art and can be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding serine/threonine kinase polypeptides include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide.

Alternatively, sequences encoding a serine/threonine kinase polypeptide can be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and can be used to synthesize RNA probes *in vitro* by addition of labeled nucleotides and an appropriate RNA polymerase such as T7, T3, or SP6. These procedures can be conducted using a variety of commercially available kits (Amersham Pharmacia Biotech, Promega, and US Biochemical). Suitable reporter molecules or labels which can be used for ease of detection include radionuclides, enzymes, and fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Expression and Purification of Polypeptides

Host cells transformed with nucleotide sequences encoding a serine/threonine kinase polypeptide can be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The polypeptide produced by a transformed cell can be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode serine/threonine kinase polypeptides can be designed to contain signal sequences which direct secretion of soluble serine/threonine kinase polypeptides through a prokaryotic or eukaryotic cell membrane or which direct the membrane insertion of membrane-bound serine/threonine kinase polypeptide.

As discussed above, other constructions can be used to join a sequence encoding a serine/threonine kinase polypeptide to a nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). Inclusion of cleavable linker sequences such as those specific for Factor Xa or enterokinase (Invitrogen, San Diego, CA) between the purification

domain and the serine/threonine kinase polypeptide also can be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing a serine/threonine kinase polypeptide and 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification by IMAC (immobilized metal ion affinity chromatography, as described in Porath *et al.*, *Prot. Exp. Purif. 3*, 263-281, 1992), while the enterokinase cleavage site provides a means for purifying the serine/threonine kinase polypeptide from the fusion protein. Vectors that contain fusion proteins are disclosed in Kroll *et al.*, *DNA Cell Biol. 12*, 441-453, 1993.

Chemical Synthesis

Sequences encoding a serine/threonine kinase polypeptide can be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers *et al.*, *Nucl. Acids Res. Symp. Ser.* 215-223, 1980; Horn *et al. Nucl. Acids Res. Symp. Ser.* 225-232, 1980). Alternatively, a serine/threonine kinase polypeptide itself can be produced using chemical methods to synthesize its amino acid sequence, such as by direct peptide synthesis using solid-phase techniques (Merrifield, *J. Am. Chem. Soc. 85*, 2149-2154, 1963; Roberge *et al.*, *Science 269*, 202-204, 1995). Protein synthesis can be performed using manual techniques or by automation. Automated synthesis can be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Optionally, fragments of serine/threonine kinase polypeptides can be separately synthesized and combined using chemical methods to produce a full-length molecule.

The newly synthesized peptide can be substantially purified by preparative high performance liquid chromatography (*e.g.*, Creighton, PROTEINS: STRUCTURES AND MOLECULAR PRINCIPLES, WH Freeman and Co., New York, N.Y., 1983). The composition of a synthetic serine/threonine kinase polypeptide can be confirmed by amino acid analysis or sequencing (*e.g.*, the Edman degradation procedure; *see* Creighton, *supra*). Additionally, any portion of the amino acid sequence of the

serine/threonine kinase polypeptide can be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins to produce a variant polypeptide or a fusion protein.

Production of Altered Polypeptides

As will be understood by those of skill in the art, it may be advantageous to produce serine/threonine kinase polypeptide-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce an RNA transcript having desirable properties, such as a half-life that is longer than that of a transcript generated from the naturally occurring sequence.

The nucleotide sequences disclosed herein can be engineered using methods generally known in the art to alter serine/threonine kinase polypeptide-encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the polypeptide or mRNA product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides can be used to engineer the nucleotide sequences. For example, site-directed mutagenesis can be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, introduce mutations, and so forth.

Antibodies

Any type of antibody known in the art can be generated to bind specifically to an epitope of a serine/threonine kinase polypeptide. "Antibody" as used herein includes intact immunoglobulin molecules, as well as fragments thereof, such as Fab, $F(ab')_2$, and Fv, which are capable of binding an epitope of a serine/threonine kinase polypeptide. Typically, at least 6, 8, 10, or 12 contiguous amino acids are required to

form an epitope. However, epitopes which involve non-contiguous amino acids may require more, *e.g.*, at least 15, 25, or 50 amino acids.

An antibody which specifically binds to an epitope of a serine/threonine kinase polypeptide can be used therapeutically, as well as in immunochemical assays, such as Western blots, ELISAs, radioimmunoassays, immunohistochemical assays, immunoprecipitations, or other immunochemical assays known in the art. Various immunoassays can be used to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays are well known in the art. Such immunoassays typically involve the measurement of complex formation between an immunogen and an antibody that specifically binds to the immunogen.

Typically, an antibody which specifically binds to a serine/threonine kinase polypeptide provides a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in an immunochemical assay. Preferably, antibodies which specifically bind to serine/threonine kinase polypeptides do not detect other proteins in immunochemical assays and can immunoprecipitate a serine/threonine kinase polypeptide from solution.

Human serine/threonine kinase polypeptides can be used to immunize a mammal, such as a mouse, rat, rabbit, guinea pig, monkey, or human, to produce polyclonal antibodies. If desired, a serine/threonine kinase polypeptide can be conjugated to a carrier protein, such as bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin. Depending on the host species, various adjuvants can be used to increase the immunological response. Such adjuvants include, but are not limited to, Freund's adjuvant, mineral gels (*e.g.*, aluminum hydroxide), and surface active substances (*e.g.* lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol). Among adjuvants used in humans, BCG (*bacilli Calmette-Guerin*) and *Corynebacterium parvum* are especially useful.

Monoclonal antibodies that specifically bind to a serine/threonine kinase polypeptide can be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These techniques include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique (Kohler *et al.*, *Nature 256*, 495-497, 1985; Kozbor *et al.*, *J. Immunol. Methods 81*, 31-42, 1985; Cote *et al.*, *Proc. Natl. Acad. Sci. 80*, 2026-2030, 1983; Cole *et al.*, *Mol. Cell Biol. 62*, 109-120, 1984).

In addition, techniques developed for the production of "chimeric antibodies," the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used (Morrison *et al.*, *Proc. Natl. Acad. Sci. 81*, 6851-6855, 1984; Neuberger *et al.*, *Nature 312*, 604-608, 1984; Takeda *et al.*, *Nature 314*, 452-454, 1985). Monoclonal and other antibodies also can be "humanized" to prevent a patient from mounting an immune response against the antibody when it is used therapeutically. Such antibodies may be sufficiently similar in sequence to human antibodies to be used directly in therapy or may require alteration of a few key residues. Sequence differences between rodent antibodies and human sequences can be minimized by replacing residues which differ from those in the human sequences by site directed mutagenesis of individual residues or by grating of entire complementarity determining regions. Alternatively, humanized antibodies can be produced using recombinant methods, as described in GB2188638B. Antibodies that specifically bind to a serine/threonine kinase polypeptide can contain antigen binding sites which are either partially or fully humanized, as disclosed in U.S. 5,565,332.

Alternatively, techniques described for the production of single chain antibodies can be adapted using methods known in the art to produce single chain antibodies that specifically bind to serine/threonine kinase polypeptides. Antibodies with related specificity, but of distinct idiotypic composition, can be generated by chain shuffling from random combinatorial immunoglobin libraries (Burton, *Proc. Natl. Acad. Sci. 88*, 11120-23, 1991).

Single-chain antibodies also can be constructed using a DNA amplification method, such as PCR, using hybridoma cDNA as a template (Thirion *et al.*, 1996, *Eur. J. Cancer Prev. 5*, 507-11). Single-chain antibodies can be mono- or bispecific, and can be bivalent or tetravalent. Construction of tetravalent, bispecific single-chain antibodies is taught, for example, in Coloma & Morrison, 1997, *Nat. Biotechnol. 15*, 159-63. Construction of bivalent, bispecific single-chain antibodies is taught in Mallender & Voss, 1994, *J. Biol. Chem. 269*, 199-206.

A nucleotide sequence encoding a single-chain antibody can be constructed using manual or automated nucleotide synthesis, cloned into an expression construct using standard recombinant DNA methods, and introduced into a cell to express the coding sequence, as described below. Alternatively, single-chain antibodies can be produced directly using, for example, filamentous phage technology (Verhaar *et al.*, 1995, *Int. J. Cancer 61*, 497-501; Nicholls *et al.*, 1993, *J. Immunol. Meth. 165*, 81-91).

Antibodies which specifically bind to serine/threonine kinase polypeptides also can be produced by inducing *in vivo* production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature (Orlandi *et al.*, *Proc. Natl. Acad. Sci. 86*, 3833-3837, 1989; Winter *et al.*, *Nature 349*, 293-299, 1991).

Other types of antibodies can be constructed and used therapeutically in methods of the invention. For example, chimeric antibodies can be constructed as disclosed in WO 93/03151. Binding proteins which are derived from immunoglobulins and which are multivalent and multispecific, such as the "diabodies" described in WO 94/13804, also can be prepared.

Antibodies according to the invention can be purified by methods well known in the art. For example, antibodies can be affinity purified by passage over a column to

which a serine/threonine kinase polypeptide is bound. The bound antibodies can then be eluted from the column using a buffer with a high salt concentration.

Antisense Oligonucleotides

Antisense oligonucleotides are nucleotide sequences that are complementary to a specific DNA or RNA sequence. Once introduced into a cell, the complementary nucleotides combine with natural sequences produced by the cell to form complexes and block either transcription or translation. Preferably, an antisense oligonucleotide is at least 11 nucleotides in length, but can be at least 12, 15, 20, 25, 30, 35, 40, 45, or 50 or more nucleotides long. Longer sequences also can be used. Antisense oligonucleotide molecules can be provided in a DNA construct and introduced into a cell as described above to decrease the level of serine/threonine kinase gene products in the cell.

Antisense oligonucleotides can be deoxyribonucleotides, ribonucleotides, or a combination of both. Oligonucleotides can be synthesized manually or by an automated synthesizer, by covalently linking the 5' end of one nucleotide with the 3' end of another nucleotide with non-phosphodiester internucleotide linkages such alkylphosphonates, phosphorothioates, phosphorodithioates, alkylphosphonothioates, alkylphosphonates, phosphoramidates, phosphate esters, carbamates, acetamidate, carboxymethyl esters, carbonates, and phosphate triesters. *See* Brown, *Meth. Mol. Biol. 20*, 1-8, 1994; Sonveaux, *Meth. Mol. Biol. 26*, 1-72, 1994; Uhlmann *et al.*, *Chem. Rev. 90*, 543-583, 1990.

Modifications of serine/threonine kinase gene expression can be obtained by designing antisense oligonucleotides that will form duplexes to the control, 5', or regulatory regions of the serine/threonine kinase gene. Oligonucleotides derived from the transcription initiation site, *e.g.*, between positions -10 and +10 from the start site, are preferred. Similarly, inhibition can be achieved using "triple helix" base-pairing methodology. Triple helix pairing is useful because it causes inhibition

of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or chaperons. Therapeutic advances using triplex DNA have been described in the literature (*e.g.*, Gee *et al.*, in Huber & Carr, MOLECULAR AND IMMUNOLOGIC APPROACHES, Futura Publishing Co., Mt. Kisco, N.Y., 1994). An antisense oligonucleotide also can be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Precise complementarity is not required for successful complex formation between an antisense oligonucleotide and the complementary sequence of a serine/threonine kinase polynucleotide. Antisense oligonucleotides which comprise, for example, 2, 3, 4, or 5 or more stretches of contiguous nucleotides which are precisely complementary to a serine/threonine kinase polynucleotide, each separated by a stretch of contiguous nucleotides which are not complementary to adjacent serine/threonine kinase nucleotides, can provide sufficient targeting specificity for serine/threonine kinase mRNA. Preferably, each stretch of complementary contiguous nucleotides is at least 4, 5, 6, 7, or 8 or more nucleotides in length. Non-complementary intervening sequences are preferably 1, 2, 3, or 4 nucleotides in length. One skilled in the art can easily use the calculated melting point of an antisense-sense pair to determine the degree of mismatching which will be tolerated between a particular antisense oligonucleotide and a particular serine/threonine kinase polynucleotide sequence.

Antisense oligonucleotides can be modified without affecting their ability to hybridize to a serine/threonine kinase polynucleotide. These modifications can be internal or at one or both ends of the antisense molecule. For example, inter-nucleoside phosphate linkages can be modified by adding cholesteryl or diamine moieties with varying numbers of carbon residues between the amino groups and terminal ribose. Modified bases and/or sugars, such as arabinose instead of ribose, or a 3', 5'-substituted oligonucleotide in which the 3' hydroxyl group or the 5' phosphate group are substituted, also can be employed in a modified antisense oligonucleotide. These modified oligonucleotides can be prepared by methods well

known in the art. *See, e.g.*, Agrawal *et al.*, *Trends Biotechnol. 10*, 152-158, 1992; Uhlmann *et al.*, *Chem. Rev. 90*, 543-584, 1990; Uhlmann *et al.*, *Tetrahedron. Lett. 215*, 3539-3542, 1987.

Ribozymes

Ribozymes are RNA molecules with catalytic activity. *See*, *e.g.*, Cech, *Science 236*, 1532-1539; 1987; Cech, *Ann. Rev. Biochem. 59*, 543-568; 1990, Cech, *Curr. Opin. Struct. Biol. 2*, 605-609; 1992, Couture & Stinchcomb, *Trends Genet. 12*, 510-515, 1996. Ribozymes can be used to inhibit gene function by cleaving an RNA sequence, as is known in the art (*e.g.*, Haseloff *et al.*, U.S. Patent 5,641,673). The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. Examples include engineered hammerhead motif ribozyme molecules that can specifically and efficiently catalyze endonucleolytic cleavage of specific nucleotide sequences.

The coding sequence of a serine/threonine kinase polynucleotide can be used to generate ribozymes that will specifically bind to mRNA transcribed from the serine/threonine kinase polynucleotide. Methods of designing and constructing ribozymes which can cleave other RNA molecules in trans in a highly sequence specific manner have been developed and described in the art (*see* Haseloff *et al.* *Nature 334*, 585-591, 1988). For example, the cleavage activity of ribozymes can be targeted to specific RNAs by engineering a discrete "hybridization" region into the ribozyme. The hybridization region contains a sequence complementary to the target RNA and thus specifically hybridizes with the target (see, for example, Gerlach *et al.*, EP 321,201).

Specific ribozyme cleavage sites within a serine/threonine kinase RNA target can be identified by scanning the target molecule for ribozyme cleavage sites which include the following sequences: GUA, GUU, and GUC. Once identified, short RNA

sequences of between 15 and 20 ribonucleotides corresponding to the region of the target RNA containing the cleavage site can be evaluated for secondary structural features which may render the target inoperable. Suitability of candidate serine/threonine kinase RNA targets also can be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays. Longer complementary sequences can be used to increase the affinity of the hybridization sequence for the target. The hybridizing and cleavage regions of the ribozyme can be integrally related such that upon hybridizing to the target RNA through the complementary regions, the catalytic region of the ribozyme can cleave the target.

Ribozymes can be introduced into cells as part of a DNA construct. Mechanical methods, such as microinjection, liposome-mediated transfection, electroporation, or calcium phosphate precipitation, can be used to introduce a ribozyme-containing DNA construct into cells in which it is desired to decrease serine/threonine kinase expression. Alternatively, if it is desired that the cells stably retain the DNA construct, the construct can be supplied on a plasmid and maintained as a separate element or integrated into the genome of the cells, as is known in the art. A ribozyme-encoding DNA construct can include transcriptional regulatory elements, such as a promoter element, an enhancer or UAS element, and a transcriptional terminator signal, for controlling transcription of ribozymes in the cells.

As taught in Haseloff *et al.*, U.S. Patent 5,641,673, ribozymes can be engineered so that ribozyme expression will occur in response to factors that induce expression of a target gene. Ribozymes also can be engineered to provide an additional level of regulation, so that destruction of mRNA occurs only when both a ribozyme and a target gene are induced in the cells.

Differentially Expressed Genes

Described herein are methods for the identification of genes whose products interact with human serine/threonine kinase. Such genes may represent genes that are differentially expressed in disorders including, but not limited to, cancer, diabetes, CNS disorders, and COPD. Further, such genes may represent genes that are differentially regulated in response to manipulations relevant to the progression or treatment of such diseases. Additionally, such genes may have a temporally modulated expression, increased or decreased at different stages of tissue or organism development. A differentially expressed gene may also have its expression modulated under control versus experimental conditions. In addition, the human serine/threonine kinase gene or gene product may itself be tested for differential expression.

The degree to which expression differs in a normal versus a diseased state need only be large enough to be visualized via standard characterization techniques such as differential display techniques. Other such standard characterization techniques by which expression differences may be visualized include but are not limited to, quantitative RT (reverse transcriptase), PCR, and Northern analysis.

Identification of Differentially Expressed Genes

To identify differentially expressed genes total RNA or, preferably, mRNA is isolated from tissues of interest. For example, RNA samples are obtained from tissues of experimental subjects and from corresponding tissues of control subjects. Any RNA isolation technique that does not select against the isolation of mRNA may be utilized for the purification of such RNA samples. See, for example, Ausubel *et al.*, ed., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, Inc. New York, 1987-1993. Large numbers of tissue samples may readily be processed using techniques well known to those of skill in the art, such as, for example, the single-step RNA isolation process of Chomczynski, U.S. Patent 4,843,155.

Transcripts within the collected RNA samples that represent RNA produced by differentially expressed genes are identified by methods well known to those of skill in the art. They include, for example, differential screening (Tedder *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 85*, 208-12, 1988), subtractive hybridization (Hedrick *et al.*, *Nature 308*, 149-53; Lee *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 88*, 2825, 1984), and, preferably, differential display (Liang & Pardee, *Science 257*, 967-71, 1992; U.S. Patent 5,262,311).

The differential expression information may itself suggest relevant methods for the treatment of disorders involving the human serine/threonine kinase. For example, treatment may include a modulation of expression of the differentially expressed genes and/or the gene encoding the human serine/threonine kinase. The differential expression information may indicate whether the expression or activity of the differentially expressed gene or gene product or the human serine/threonine kinase gene or gene product are up-regulated or down-regulated.

Screening Methods

The invention provides assays for screening test compounds that bind to or modulate the activity of a serine/threonine kinase polypeptide or a serine/threonine kinase polynucleotide. A test compound preferably binds to a serine/threonine kinase polypeptide or polynucleotide. More preferably, a test compound decreases or increases enzymatic activity by at least about 10, preferably about 50, more preferably about 75, 90, or 100% relative to the absence of the test compound.

Test Compounds

Test compounds can be pharmacologic agents already known in the art or can be compounds previously unknown to have any pharmacological activity. The compounds can be naturally occurring or designed in the laboratory. They can be

isolated from microorganisms, animals, or plants, and can be produced recombinantly, or synthesized by chemical methods known in the art. If desired, test compounds can be obtained using any of the numerous combinatorial library methods known in the art, including but not limited to, biological libraries, spatially addressable parallel solid phase or solution phase libraries, synthetic library methods requiring deconvolution, the "one-bead one-compound" library method, and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide libraries, while the other four approaches are applicable to polypeptide, non-peptide oligomer, or small molecule libraries of compounds. *See* Lam, *Anticancer Drug Des. 12*, 145, 1997.

Methods for the synthesis of molecular libraries are well known in the art (*see*, for example, DeWitt *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 90*, 6909, 1993; Erb *et al. Proc. Natl. Acad. Sci. U.S.A. 91*, 11422, 1994; Zuckermann *et al.*, *J. Med. Chem. 37*, 2678, 1994; Cho *et al.*, *Science 261*, 1303, 1993; Carell *et al.*, *Angew. Chem. Int. Ed. Engl. 33*, 2059, 1994; Carell *et al.*, *Angew. Chem. Int. Ed. Engl. 33*, 2061; Gallop *et al.*, *J. Med. Chem. 37*, 1233, 1994). Libraries of compounds can be presented in solution (*see*, *e.g.*, Houghten, *BioTechniques 13*, 412-421, 1992), or on beads (Lam, *Nature 354*, 82-84, 1991), chips (Fodor, *Nature 364*, 555-556, 1993), bacteria or spores (Ladner, U.S. Patent 5,223,409), plasmids (Cull *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 89*, 1865-1869, 1992), or phage (Scott & Smith, *Science 249*, 386-390, 1990; Devlin, *Science 249*, 404-406, 1990); Cwirla *et al.*, *Proc. Natl. Acad. Sci. 97*, 6378-6382, 1990; Felici, *J. Mol. Biol. 222*, 301-310, 1991; and Ladner, U.S. Patent 5,223,409).

High Throughput Screening

Test compounds can be screened for the ability to bind to serine/threonine kinase polypeptides or polynucleotides or to affect serine/threonine kinase activity or serine/threonine kinase gene expression using high throughput screening. Using high throughput screening, many discrete compounds can be tested in parallel so that large numbers of test compounds can be quickly screened. The most widely established

techniques utilize 96-well microtiter plates. The wells of the microtiter plates typically require assay volumes that range from 50 to 500 µl. In addition to the plates, many instruments, materials, pipettors, robotics, plate washers, and plate readers are commercially available to fit the 96-well format.

Alternatively, "free format assays," or assays that have no physical barrier between samples, can be used. For example, an assay using pigment cells (melanocytes) in a simple homogeneous assay for combinatorial peptide libraries is described by Jayawickreme *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 19,* 1614-18 (1994). The cells are placed under agarose in petri dishes, then beads that carry combinatorial compounds are placed on the surface of the agarose. The combinatorial compounds are partially released the compounds from the beads. Active compounds can be visualized as dark pigment areas because, as the compounds diffuse locally into the gel matrix, the active compounds cause the cells to change colors.

Another example of a free format assay is described by Chelsky, "Strategies for Screening Combinatorial Libraries: Novel and Traditional Approaches," reported at the First Annual Conference of The Society for Biomolecular Screening in Philadelphia, Pa. (Nov. 7-10, 1995). Chelsky placed a simple homogenous enzyme assay for carbonic anhydrase inside an agarose gel such that the enzyme in the gel would cause a color change throughout the gel. Thereafter, beads carrying combinatorial compounds via a photolinker were placed inside the gel and the compounds were partially released by UV-light. Compounds that inhibited the enzyme were observed as local zones of inhibition having less color change.

Yet another example is described by Salmon *et al.*, *Molecular Diversity 2*, 57-63 (1996). In this example, combinatorial libraries were screened for compounds that had cytotoxic effects on cancer cells growing in agar.

Another high throughput screening method is described in Beutel *et al.*, U.S. Patent 5,976,813. In this method, test samples are placed in a porous matrix. One or more

assay components are then placed within, on top of, or at the bottom of a matrix such as a gel, a plastic sheet, a filter, or other form of easily manipulated solid support. When samples are introduced to the porous matrix they diffuse sufficiently slowly, such that the assays can be performed without the test samples running together.

Binding Assays

For binding assays, the test compound is preferably a small molecule that binds to and occupies, for example, the active site of the serine/threonine kinase polypeptide, such that normal biological activity is prevented. Examples of such small molecules include, but are not limited to, small peptides or peptide-like molecules.

In binding assays, either the test compound or the serine/threonine kinase polypeptide can comprise a detectable label, such as a fluorescent, radioisotopic, chemiluminescent, or enzymatic label, such as horseradish peroxidase, alkaline phosphatase, or luciferase. Detection of a test compound that is bound to the serine/threonine kinase polypeptide can then be accomplished, for example, by direct counting of radioemmission, by scintillation counting, or by determining conversion of an appropriate substrate to a detectable product.

Alternatively, binding of a test compound to a serine/threonine kinase polypeptide can be determined without labeling either of the interactants. For example, a microphysiometer can be used to detect binding of a test compound with a serine/threonine kinase polypeptide. A microphysiometer (*e.g.*, Cytosensor™) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between a test compound and a serine/threonine kinase polypeptide (McConnell *et al.*, *Science 257*, 1906-1912, 1992).

Determining the ability of a test compound to bind to a serine/threonine kinase polypeptide also can be accomplished using a technology such as real-time Bimolecular Interaction Analysis (BIA) (Sjolander & Urbaniczky, *Anal. Chem. 63*, 2338-2345, 1991, and Szabo *et al.*, *Curr. Opin. Struct. Biol. 5*, 699-705, 1995). BIA is a technology for studying biospecific interactions in real time, without labeling any of the interactants (*e.g.*, BIAcore™). Changes in the optical phenomenon surface plasmon resonance (SPR) can be used as an indication of real-time reactions between biological molecules.

In yet another aspect of the invention, a serine/threonine kinase polypeptide can be used as a "bait protein" in a two-hybrid assay or three-hybrid assay (see, *e.g.*, U.S. Patent 5,283,317; Zervos *et al.*, *Cell 72*, 223-232, 1993; Madura *et al.*, *J. Biol. Chem. 268*, 12046-12054, 1993; Bartel *et al.*, *BioTechniques 14*, 920-924, 1993; Iwabuchi *et al.*, *Oncogene 8*, 1693-1696, 1993; and Brent W094/10300), to identify other proteins which bind to or interact with the serine/threonine kinase polypeptide and modulate its activity.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. For example, in one construct, polynucleotide encoding a serine/threonine kinase polypeptide can be fused to a polynucleotide encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct a DNA sequence that encodes an unidentified protein ("prey" or "sample") can be fused to a polynucleotide that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact *in vivo* to form an protein-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ), which is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected, and cell colonies containing the

functional transcription factor can be isolated and used to obtain the DNA sequence encoding the protein that interacts with the serine/threonine kinase polypeptide.

It may be desirable to immobilize either the serine/threonine kinase polypeptide (or polynucleotide) or the test compound to facilitate separation of bound from unbound forms of one or both of the interactants, as well as to accommodate automation of the assay. Thus, either the serine/threonine kinase polypeptide (or polynucleotide) or the test compound can be bound to a solid support. Suitable solid supports include, but are not limited to, glass or plastic slides, tissue culture plates, microtiter wells, tubes, silicon chips, or particles such as beads (including, but not limited to, latex, polystyrene, or glass beads). Any method known in the art can be used to attach the enzyme polypeptide (or polynucleotide) or test compound to a solid support, including use of covalent and non-covalent linkages, passive absorption, or pairs of binding moieties attached respectively to the polypeptide (or polynucleotide) or test compound and the solid support. Test compounds are preferably bound to the solid support in an array, so that the location of individual test compounds can be tracked. Binding of a test compound to a serine/threonine kinase polypeptide (or polynucleotide) can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and microcentrifuge tubes.

In one embodiment, the serine/threonine kinase polypeptide is a fusion protein comprising a domain that allows the serine/threonine kinase polypeptide to be bound to a solid support. For example, glutathione-S-transferase fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, Mo.) or glutathione derivatized microtiter plates, which are then combined with the test compound or the test compound and the non-adsorbed serine/threonine kinase polypeptide; the mixture is then incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components. Binding of the interactants can be determined either directly or indirectly, as

described above. Alternatively, the complexes can be dissociated from the solid support before binding is determined.

Other techniques for immobilizing proteins or polynucleotides on a solid support also can be used in the screening assays of the invention. For example, either a serine/threonine kinase polypeptide (or polynucleotide) or a test compound can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated serine/threonine kinase polypeptides (or polynucleotides) or test compounds can be prepared from biotin-NHS(N-hydroxysuccinimide) using techniques well known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.) and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies which specifically bind to a serine/threonine kinase polypeptide, polynucleotide, or a test compound, but which do not interfere with a desired binding site, such as the active site of the serine/threonine kinase polypeptide, can be derivatized to the wells of the plate. Unbound target or protein can be trapped in the wells by antibody conjugation.

Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies which specifically bind to the serine/threonine kinase polypeptide or test compound, enzyme-linked assays which rely on detecting an activity of the serine/threonine kinase polypeptide, and SDS gel electrophoresis under non-reducing conditions.

Screening for test compounds which bind to a serine/threonine kinase polypeptide or polynucleotide also can be carried out in an intact cell. Any cell which comprises a serine/threonine kinase polypeptide or polynucleotide can be used in a cell-based assay system. A serine/threonine kinase polynucleotide can be naturally occurring in the cell or can be introduced using techniques such as those described above. Binding of the test compound to a serine/threonine kinase polypeptide or polynucleotide is determined as described above.

Enzyme Assays

Test compounds can be tested for the ability to increase or decrease the enzymatic activity of a human serine/threonine kinase polypeptide. Enzymatic activity can be measured, for example, as described in Trost *et al.*, *J. Biol. Chem. 275*, 7373-77, 2000; Hayashi *et al.*, *Biochem. Biophys. Res. Commun. 264*, 449-56, 1999; Masure *et al.*, *Eur. J. Biochem. 265*, 353-60, 1999; and Mukhopadhyay *et al.*, *J. Bacteriol. 181*, 6615-22, 1999.

Enzyme assays can be carried out after contacting either a purified serine/threonine kinase polypeptide, a cell membrane preparation, or an intact cell with a test compound. A test compound that decreases an enzymatic activity of a serine/threonine kinase polypeptide by at least about 10, preferably about 50, more preferably about 75, 90, or 100% is identified as a potential therapeutic agent for decreasing serine/threonine kinase activity. A test compound which increases an enzymatic activity of a human serine/threonine kinase polypeptide by at least about 10, preferably about 50, more preferably about 75, 90, or 100% is identified as a potential therapeutic agent for increasing human serine/threonine kinase activity.

Gene Expression

In another embodiment, test compounds that increase or decrease serine/threonine kinase gene expression are identified. A serine/threonine kinase polynucleotide is contacted with a test compound, and the expression of an RNA or polypeptide product of the serine/threonine kinase polynucleotide is determined. The level of expression of appropriate mRNA or polypeptide in the presence of the test compound is compared to the level of expression of mRNA or polypeptide in the absence of the test compound. The test compound can then be identified as a modulator of expression based on this comparison. For example, when expression of mRNA or polypeptide is greater in the presence of the test compound than in its absence, the

test compound is identified as a stimulator or enhancer of the mRNA or polypeptide expression. Alternatively, when expression of the mRNA or polypeptide is less in the presence of the test compound than in its absence, the test compound is identified as an inhibitor of the mRNA or polypeptide expression.

The level of serine/threonine kinase mRNA or polypeptide expression in the cells can be determined by methods well known in the art for detecting mRNA or polypeptide. Either qualitative or quantitative methods can be used. The presence of polypeptide products of a serine/threonine kinase polynucleotide can be determined, for example, using a variety of techniques known in the art, including immunochemical methods such as radioimmunoassay, Western blotting, and immunohistochemistry. Alternatively, polypeptide synthesis can be determined *in vivo*, in a cell culture, or in an *in vitro* translation system by detecting incorporation of labeled amino acids into a serine/threonine kinase polypeptide.

Such screening can be carried out either in a cell-free assay system or in an intact cell. Any cell that expresses a serine/threonine kinase polynucleotide can be used in a cell-based assay system. The serine/threonine kinase polynucleotide can be naturally occurring in the cell or can be introduced using techniques such as those described above. Either a primary culture or an established cell line, such as CHO or human embryonic kidney 293 cells, can be used.

Pharmaceutical Compositions

The invention also provides pharmaceutical compositions that can be administered to a patient to achieve a therapeutic effect. Pharmaceutical compositions of the invention can comprise, for example, a serine/threonine kinase polypeptide, serine/threonine kinase polynucleotide, ribozymes or antisense oligonucleotides, antibodies which specifically bind to a serine/threonine kinase polypeptide, or mimetics, activators, or inhibitors of a serine/threonine kinase polypeptide activity. The compositions can be administered alone or in combination with at least one other

agent, such as stabilizing compound, which can be administered in any sterile, biocompatible pharmaceutical carrier, including, but not limited to, saline, buffered saline, dextrose, and water. The compositions can be administered to a patient alone, or in combination with other agents, drugs or hormones.

In addition to the active ingredients, these pharmaceutical compositions can contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries that facilitate processing of the active compounds into preparations which can be used pharmaceutically. Pharmaceutical compositions of the invention can be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, parenteral, topical, sublingual, or rectal means. Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions, and the like, for ingestion by the patient.

Pharmaceutical preparations for oral use can be obtained through combination of active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are carbohydrate or protein fillers, such as sugars, including lactose, sucrose, mannitol, or sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose, such as methyl cellulose, hydroxy-propylmethyl-cellulose, or sodium carboxymethylcellulose; gums including arabic and tragacanth; and proteins such as gelatin and collagen. If desired, disintegrating or solubilizing agents can be added, such as the cross-linked polyvinyl pyrrolidone, agar, alginic acid, or a salt thereof, such as sodium alginate.

Dragee cores can be used in conjunction with suitable coatings, such as concentrated sugar solutions, which also can contain gum arabic, talc, polyvinylpyrrolidone,

carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments can be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, *i.e.*, dosage.

Pharmaceutical preparations that can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating, such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with a filler or binders, such as lactose or starches, lubricants, such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds can be dissolved or suspended in suitable liquids, such as fatty oils, liquid, or liquid polyethylene glycol with or without stabilizers.

Pharmaceutical formulations suitable for parenteral administration can be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions can contain substances that increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds can be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Non-lipid polycationic amino polymers also can be used for delivery. Optionally, the suspension also can contain suitable stabilizers or agents that increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

The pharmaceutical compositions of the present invention can be manufactured in a manner that is known in the art, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or

lyophilizing processes. The pharmaceutical composition can be provided as a salt and can be formed with many acids, including but not limited to, hydrochloric, sulfuric, acetic, lactic, tartaric, malic, succinic, etc. Salts tend to be more soluble in aqueous or other protonic solvents than are the corresponding free base forms. In other cases, the preferred preparation can be a lyophilized powder which can contain any or all of the following: 1-50 mM histidine, 0.1%-2% sucrose, and 2-7% mannitol, at a pH range of 4.5 to 5.5, that is combined with buffer prior to use.

Further details on techniques for formulation and administration can be found in the latest edition of REMINGTON'S PHARMACEUTICAL SCIENCES (Maack Publishing Co., Easton, Pa.). After pharmaceutical compositions have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated condition. Such labeling would include amount, frequency, and method of administration.

Therapeutic Indications and Methods

Human serine/threonine kinase can be regulated to treat cancer, diabetes, CNS disorders, and COPD.

Cancer is a disease fundamentally caused by oncogenic cellular transformation. There are several hallmarks of transformed cells that distinguish them from their normal counterparts and underlie the pathophysiology of cancer. These include uncontrolled cellular proliferation, unresponsiveness to normal death-inducing signals (immortalization), increased cellular motility and invasiveness, increased ability to recruit blood supply through induction of new blood vessel formation (angiogenesis), genetic instability, and dysregulated gene expression. Various combinations of these aberrant physiologies, along with the acquisition of drug-resistance frequently lead to an intractable disease state in which organ failure and patient death ultimately ensue.

Diabetes. Diabetes mellitus is a common metabolic disorder characterized by an abnormal elevation in blood glucose, alterations in lipids and abnormalities (complications) in the cardiovascular system, eye, kidney and nervous system. Diabetes is divided into two separate diseases: type 1 diabetes (juvenile onset), which results from a loss of cells which make and secrete insulin, and type 2 diabetes (adult onset), which is caused by a defect in insulin secretion and a defect in insulin action.

Type 1 diabetes is initiated by an autoimmune reaction that attacks the insulin secreting cells (beta cells) in the pancreatic islets. Agents that prevent this reaction from occurring or that stop the reaction before destruction of the beta cells has been accomplished are potential therapies for this disease. Other agents that induce beta cell proliferation and regeneration also are potential therapies.

Type II diabetes is the most common of the two diabetic conditions (6% of the population). The defect in insulin secretion is an important cause of the diabetic condition and results from an inability of the beta cell to properly detect and respond to rises in blood glucose levels with insulin release. Therapies that increase the response by the beta cell to glucose would offer an important new treatment for this disease.

The defect in insulin action in Type II diabetic subjects is another target for therapeutic intervention. Agents that increase the activity of the insulin receptor in muscle, liver, and fat will cause a decrease in blood glucose and a normalization of plasma lipids. The receptor activity can be increased by agents that directly stimulate the receptor or that increase the intracellular signals from the receptor. Other therapies can directly activate the cellular end process, *i.e.* glucose transport or various enzyme systems, to generate an insulin-like effect and therefore a produce beneficial outcome. Because overweight subjects have a greater susceptibility to Type II diabetes, any agent that reduces body weight is a possible therapy.

Both Type I and Type diabetes can be treated with agents that mimic insulin action or that treat diabetic complications by reducing blood glucose levels. Likewise, agents that reduces new blood vessel growth can be used to treat the eye complications that develop in both diseases.

CNS disorders. Central and peripheral nervous system disorders also can be treated, such as primary and secondary disorders after brain injury, disorders of mood, anxiety disorders, disorders of thought and volition, disorders of sleep and wakefulness, diseases of the motor unit, such as neurogenic and myopathic disorders, neurodegenerative disorders such as Alzheimer's and Parkinson's disease, and processes of peripheral and chronic pain.

Pain that is associated with CNS disorders also can be treated by regulating the activity of human serine/threonine kinase. Pain which can be treated includes that associated with central nervous system disorders, such as multiple sclerosis, spinal cord injury, sciatica, failed back surgery syndrome, traumatic brain injury, epilepsy, Parkinson's disease, post-stroke, and vascular lesions in the brain and spinal cord (*e.g.*, infarct, hemorrhage, vascular malformation). Non-central neuropathic pain includes that associated with post mastectomy pain, reflex sympathetic dystrophy (RSD), trigeminal neuralgiaradioculopathy, post-surgical pain, HIV/AIDS related pain, cancer pain, metabolic neuropathies (*e.g.*, diabetic neuropathy, vasculitic neuropathy secondary to connective tissue disease), paraneoplastic polyneuropathy associated, for example, with carcinoma of lung, or leukemia, or lymphoma, or carcinoma of prostate, colon or stomach, trigeminal neuralgia, cranial neuralgias, and post-herpetic neuralgia. Pain associated with cancer and cancer treatment also can be treated, as can headache pain (for example, migraine with aura, migraine without aura, and other migraine disorders), episodic and chronic tension-type headache, tension-type like headache, cluster headache, and chronic paroxysmal hemicrania.

This invention further pertains to the use of novel agents identified by the screening assays described above. Accordingly, it is within the scope of this invention to use a test compound identified as described herein in an appropriate animal model.

COPD. Chronic obstructive pulmonary (or airways) disease (COPD) is a condition defined physiologically as airflow obstruction that generally results from a mixture of emphysema and peripheral airway obstruction due to chronic bronchitis (Senior & Shapiro, *Pulmonary Diseases and Disorders*, 3d ed., New York, McGraw-Hill, 1998, pp. 659-681, 1998; Barnes, *Chest 117*, 10S-14S, 2000). Emphysema is characterized by destruction of alveolar walls leading to abnormal enlargement of the air spaces of the lung. Chronic bronchitis is defined clinically as the presence of chronic productive cough for three months in each of two successive years. In COPD, airflow obstruction is usually progressive and is only partially reversible. By far the most important risk factor for development of COPD is cigarette smoking, although the disease does occur in non-smokers.

Chronic inflammation of the airways is a key pathological feature of COPD (Senior & Shapiro, 1998). The inflammatory cell population comprises increased numbers of macrophages, neutrophils, and $CD8^+$ lymphocytes. Inhaled irritants, such as cigarette smoke, activate macrophages which are resident in the respiratory tract, as well as epithelial cells leading to release of chemokines (*e.g.*, interleukin-8) and other chemotactic factors. These chemotactic factors act to increase the neutrophil/monocyte trafficking from the blood into the lung tissue and airways. Neutrophils and monocytes recruited into the airways can release a variety of potentially damaging mediators such as proteolytic enzymes and reactive oxygen species. Matrix degradation and emphysema, along with airway wall thickening, surfactant dysfunction, and mucus hypersecretion, all are potential sequelae of this inflammatory response that lead to impaired airflow and gas exchange.

Protein kinases are signal transducing enzymes that phosphorylate proteins, including other kinases, and, along with protein phosphatases, regulate the level and extent of

protein phosphorylation and activation. Intracellular signalling pathways have important roles in inflammatory processes. These pathways may be activated by cytokines, oxidant stress and other inflammatory mediators (reviewed in Kyraikis and Avruch, 1996 and 2001). For example, the pro-inflammatory cytokines, tumor necrosis factor α (TNFα) and interleukin-1 activate the protein ser/thr kinases c-Jun-NH2-terminal kinase (JNK) and p38 mitogen-activated protein (MAP) kinase, leading to activation of AP-1 and IKB kinase (IKK), which, in turn, leads to activation of the transcription factor NFKB. Activation of NFKB is required for the transcription of several pro-inflammatory molecules, including interleukin-8 and ICAM-1. Enzymes of the MAP kinase class may also act to increase cytokine production by stabilization of mRNA (Winzen et al., 1999).

Inhibition of specific protein kinases has been shown to elicit anti-inflammatory effects. For example, the accumulation of polymorphonuclear leukocytes in murine lung following intratracheal administration of bacterial lipopolysaccharide can be blocked by inhibition of p38 MAP kinase (Nick, et al. 2000). As a further example, aerosol delivery to rat lungs of antisense oligodeoxynucleotides to syk kinase mRNA, suppressed nitric oxide and TNFα production from alveolar macrophages stimulated with IgG-anti-IgG complexes (Stenton et al. 2000). Protein kinase subtypes are therefore attractive therapeutic targets for the attenuation of the inflammatory response in COPD. See Kyriakis, J.M. and Avruch J. Sounding the alarm: protein kinase cascades activated by stress and inflammation. J Biol Chem 1996, 271:24313-6; Kyriakis, J.M. and Avruch, J. Mammalian mitogen-activated protein kinase signal transduction pathways activated by stress and inflammation. J. Physiol. Rev. 2001, 81:807-69; Winzen, R., Kracht, M., Ritter, B., Wilhelm, A., Chen C.A., Shyu, A., Müller, M., Gaestel, M., Resch, K., and Holtmann, H. The p38 MAP kinase pathway signals for cytokine-induced mRNA stabilization via MAP kinase-activated protein kinase 2 and an AU-rich region-targeted mechanism. EMBO J. 1999, 18: 4969-4980;

Nick, J.A., Young, S.K., Brown, K.K., Avdi, N.J., Arndt, P.G., Suratt, B.T., Janes, M.S., Henson, P.M., Worthen, G.S. Role of p38 mitogen-activated protein kinase in a murine model of pulmonary inflammation. J Immunol. 2000, 164:2151-9; Stenton, G.R., Kim, M.K., Nohara, O., Chen, C.F., Hirji, N., Wills, F.L., Gilchrist, M., Hwang, P.H., Park, J.G., Finlay, W., Jones, R.L., Befus, A.D., Schreiber, A.D. Aerosolized Syk antisense suppresses Syk expression, mediator release from macrophages, and pulmonary inflammation. J Immunol 2000, 164:3790-7.

This invention further pertains to the use of novel agents identified by the screening assays described above. Accordingly, it is within the scope of this invention to use a test compound identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.*, a modulating agent, an antisense nucleic acid molecule, a specific antibody, ribozyme, or a serine/threonine kinase polypeptide binding molecule) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein.

A reagent which affects serine/threonine kinase activity can be administered to a human cell, either *in vitro* or *in vivo*, to reduce serine/threonine kinase activity. The reagent preferably binds to an expression product of a human serine/threonine kinase gene. If the expression product is a protein, the reagent is preferably an antibody. For treatment of human cells *ex vivo*, an antibody can be added to a preparation of stem cells that have been removed from the body. The cells can then be replaced in the same or another human body, with or without clonal propagation, as is known in the art.

In one embodiment, the reagent is delivered using a liposome. Preferably, the liposome is stable in the animal into which it has been administered for at least about

30 minutes, more preferably for at least about 1 hour, and even more preferably for at least about 24 hours. A liposome comprises a lipid composition that is capable of targeting a reagent, particularly a polynucleotide, to a particular site in an animal, such as a human. Preferably, the lipid composition of the liposome is capable of targeting to a specific organ of an animal, such as the lung, liver, spleen, heart brain, lymph nodes, and skin.

A liposome useful in the present invention comprises a lipid composition that is capable of fusing with the plasma membrane of the targeted cell to deliver its contents to the cell. Preferably, the transfection efficiency of a liposome is about 0.5 μg of DNA per 16 nmole of liposome delivered to about 10^6 cells, more preferably about 1.0 μg of DNA per 16 nmole of liposome delivered to about 10^6 cells, and even more preferably about 2.0 μg of DNA per 16 nmol of liposome delivered to about 10^6 cells. Preferably, a liposome is between about 100 and 500 nm, more preferably between about 150 and 450 nm, and even more preferably between about 200 and 400 nm in diameter.

Suitable liposomes for use in the present invention include those liposomes standardly used in, for example, gene delivery methods known to those of skill in the art. More preferred liposomes include liposomes having a polycationic lipid composition and/or liposomes having a cholesterol backbone conjugated to polyethylene glycol. Optionally, a liposome comprises a compound capable of targeting the liposome to a particular cell type, such as a cell-specific ligand exposed on the outer surface of the liposome.

Complexing a liposome with a reagent such as an antisense oligonucleotide or ribozyme can be achieved using methods that are standard in the art (see, for example, U.S. Patent 5,705,151). Preferably, from about 0.1 μg to about 10 μg of polynucleotide is combined with about 8 nmol of liposomes, more preferably from about 0.5 μg to about 5 μg of polynucleotides are combined with about 8 nmol

liposomes, and even more preferably about 1.0 μg of polynucleotides is combined with about 8 nmol liposomes.

In another embodiment, antibodies can be delivered to specific tissues *in vivo* using receptor-mediated targeted delivery. Receptor-mediated DNA delivery techniques are taught in, for example, Findeis *et al. Trends in Biotechnol. 11*, 202-05 (1993); Chiou *et al.*, GENE THERAPEUTICS: METHODS AND APPLICATIONS OF DIRECT GENE TRANSFER (J.A. Wolff, ed.) (1994); Wu & Wu, *J. Biol. Chem. 263*, 621-24 (1988); Wu *et al.*, *J. Biol. Chem. 269*, 542-46 (1994); Zenke *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 87*, 3655-59 (1990); Wu *et al.*, *J. Biol. Chem. 266*, 338-42 (1991).

Determination of a Therapeutically Effective Dose

The determination of a therapeutically effective dose is well within the capability of those skilled in the art. A therapeutically effective dose refers to that amount of active ingredient which increases or decreases serine/threonine kinase activity relative to the serine/threonine kinase activity which occurs in the absence of the therapeutically effective dose.

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays or in animal models, usually mice, rabbits, dogs, or pigs. The animal model also can be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

Therapeutic efficacy and toxicity, *e.g.*, ED_{50} (the dose therapeutically effective in 50% of the population) and LD_{50} (the dose lethal to 50% of the population), can be determined by standard pharmaceutical procedures in cell cultures or experimental animals. The dose ratio of toxic to therapeutic effects is the therapeutic index, and it can be expressed as the ratio, LD_{50}/ED_{50}.

Pharmaceutical compositions that exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies is used in formulating a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject that requires treatment. Dosage and administration are adjusted to provide sufficient levels of the active ingredient or to maintain the desired effect. Factors that can be taken into account include the severity of the disease state, general health of the subject, age, weight, and gender of the subject, diet, time and frequency of administration, drug combination(s), reaction sensitivities, and tolerance/response to therapy. Long-acting pharmaceutical compositions can be administered every 3 to 4 days, every week, or once every two weeks depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts can vary from 0.1 to 100,000 micrograms, up to a total dose of about 1 g, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of poly-nucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

If the reagent is a single-chain antibody, polynucleotides encoding the antibody can be constructed and introduced into a cell either *ex vivo* or *in vivo* using well-established techniques including, but not limited to, transferrin-polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated cellular fusion, intracellular transportation of DNA-coated latex beads,

protoplast fusion, viral infection, electroporation, "gene gun," and DEAE- or calcium phosphate-mediated transfection.

Effective *in vivo* dosages of an antibody are in the range of about 5 µg to about 50 µg/kg, about 50 µg to about 5 mg/kg, about 100 µg to about 500 µg/kg of patient body weight, and about 200 to about 250 µg/kg of patient body weight. For administration of polynucleotides encoding single-chain antibodies, effective *in vivo* dosages are in the range of about 100 ng to about 200 ng, 500 ng to about 50 mg, about 1 µg to about 2 mg, about 5 µg to about 500 µg, and about 20 µg to about 100 µg of DNA.

If the expression product is mRNA, the reagent is preferably an antisense oligonucleotide or a ribozyme. Polynucleotides that express antisense oligonucleotides or ribozymes can be introduced into cells by a variety of methods, as described above.

Preferably, a reagent reduces expression of a serine/threonine kinase gene or the activity of a serine/threonine kinase polypeptide by at least about 10, preferably about 50, more preferably about 75, 90, or 100% relative to the absence of the reagent. The effectiveness of the mechanism chosen to decrease the level of expression of a serine/threonine kinase gene or the activity of a serine/threonine kinase polypeptide can be assessed using methods well known in the art, such as hybridization of nucleotide probes to serine/threonine kinase-specific mRNA, quantitative RT-PCR, immunologic detection of a serine/threonine kinase polypeptide, or measurement of serine/threonine kinase activity.

In any of the embodiments described above, any of the pharmaceutical compositions of the invention can be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy can be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents can act synergistically to effect the treatment or prevention of the various disorders described

above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

Any of the therapeutic methods described above can be applied to any subject in need of such therapy, including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

Diagnostic Methods

Human serine/threonine kinase also can be used in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases and abnormalities related to the presence of mutations in the nucleic acid sequences that encode the enzyme. For example, differences can be determined between the cDNA or genomic sequence encoding serine/threonine kinase in individuals afflicted with a disease and in normal individuals. If a mutation is observed in some or all of the afflicted individuals but not in normal individuals, then the mutation is likely to be the causative agent of the disease.

Sequence differences between a reference gene and a gene having mutations can be revealed by the direct DNA sequencing method. In addition, cloned DNA segments can be employed as probes to detect specific DNA segments. The sensitivity of this method is greatly enhanced when combined with PCR. For example, a sequencing primer can be used with a double-stranded PCR product or a single-stranded template molecule generated by a modified PCR. The sequence determination is performed by conventional procedures using radiolabeled nucleotides or by automatic sequencing procedures using fluorescent tags.

Genetic testing based on DNA sequence differences can be carried out by detection of alteration in electrophoretic mobility of DNA fragments in gels with or without denaturing agents. Small sequence deletions and insertions can be visualized, for example, by high resolution gel electrophoresis. DNA fragments of different

sequences can be distinguished on denaturing formamide gradient gels in which the mobilities of different DNA fragments are retarded in the gel at different positions according to their specific melting or partial melting temperatures (*see, e.g.*, Myers *et al.*, *Science 230*, 1242, 1985). Sequence changes at specific locations can also be revealed by nuclease protection assays, such as RNase and S 1 protection or the chemical cleavage method (*e.g.*, Cotton *et al.*, *Proc. Natl. Acad. Sci. USA 85*, 4397-4401, 1985). Thus, the detection of a specific DNA sequence can be performed by methods such as hybridization, RNase protection, chemical cleavage, direct DNA sequencing or the use of restriction enzymes and Southern blotting of genomic DNA. In addition to direct methods such as gel-electrophoresis and DNA sequencing, mutations can also be detected by *in situ* analysis.

Altered levels of serine/threonine kinase also can be detected in various tissues. Assays used to detect levels of the receptor polypeptides in a body sample, such as blood or a tissue biopsy, derived from a host are well known to those of skill in the art and include radioimmunoassays, competitive binding assays, Western blot analysis, and ELISA assays.

All patents and patent applications cited in this disclosure are expressly incorporated herein by reference. The above disclosure generally describes the present invention. A more complete understanding can be obtained by reference to the following specific examples, which are provided for purposes of illustration only and are not intended to limit the scope of the invention.

EXAMPLE 1

Detection of serine-threonine protein kinase activity

For high level expression of a FLAG-tagged serine-threonine protein kinase polypeptide, COS-1 cells are transfected with the expression vector serine-threonine protein kinase polypeptide (expressing the DNA-sequence of ID NO: 1) using the calcium phosphate method. After 5h, the cells are infected with recombinant vaccinia

virus vTF7-3 (10 plaque-forming units/cell). The cells are harvested 20h after infection and lysed in 50 mM Tris, pH 7,5, 5 mM $MgCl_2$, 0,1% Nonidet P-40, 0,5 mM dithiothreitol, 1 mM phenylmethylsulfonyl fluoride, 10 µg/ml aprotinin. Serine-threonine protein kinase polypeptide is immunoprecipitated from the lysate using anti-FLAG antibodies. In vitro kinase assay and phosphoamino acid analysis are performed in a volume of 40 µl with immunoprecipitated FLAG-serine-threonine protein kinase polypeptide in 50 mM Tris-HCl, pH 8,0, 50 mM NaCl, 5 mM $MgCl_2$, 1 mM dithiothreitol. The reaction is started by the addition of 4 µl of 1 mM ATP supplemented with 5 µCi of (-32P)ATP and incubated for 30 min at 37°C. Afterward, the samples are subjected to SDS-PAGE and phosphorylated proteins are detected by autoradiography. Histone type III-S, casein, bovine serum albumin, or myelin basic proteins are used as substrates. It is shown that the polypeptide with the amino acid sequence of SEQ ID NO: 2 has serine-threonine protein kinase activity.

EXAMPLE 2

Expression of recombinant human serine/threonine kinase

The *Pichia pastoris* expression vector pPICZB (Invitrogen, San Diego, CA) is used to produce large quantities of recombinant human serine/threonine kinase polypeptides in yeast. The serine/threonine kinase-encoding DNA sequence is derived from SEQ ID NO:1 or 4. Before insertion into vector pPICZB, the DNA sequence is modified by well known methods in such a way that it contains at its 5'-end an initiation codon and at its 3'-end an enterokinase cleavage site, a His6 reporter tag and a termination codon. Moreover, at both termini recognition sequences for restriction endonucleases are added and after digestion of the multiple cloning site of pPICZ B with the corresponding restriction enzymes the modified DNA sequence is ligated into pPICZB. This expression vector is designed for inducible expression in *Pichia pastoris*, driven by a yeast promoter. The resulting pPICZ/md-His6 vector is used to transform the yeast.

The yeast is cultivated under usual conditions in 5 liter shake flasks and the recombinantly produced protein isolated from the culture by affinity chromatography (Ni-NTA-Resin) in the presence of 8 M urea. The bound polypeptide is eluted with buffer, pH 3.5, and neutralized. Separation of the polypeptide from the His6 reporter tag is accomplished by site-specific proteolysis using enterokinase (Invitrogen, San Diego, CA) according to manufacturer's instructions. Purified human serine/threonine kinase polypeptide is obtained.

EXAMPLE 3

Identification of test compounds that bind to serine/threonine kinase polypeptides

Purified serine/threonine kinase polypeptides comprising a glutathione-S-transferase protein and absorbed onto glutathione-derivatized wells of 96-well microtiter plates are contacted with test compounds from a small molecule library at pH 7.0 in a physiological buffer solution. Human serine/threonine kinase polypeptides comprise the amino acid sequence shown in SEQ ID NO:2 or 5. The test compounds comprise a fluorescent tag. The samples are incubated for 5 minutes to one hour. Control samples are incubated in the absence of a test compound.

The buffer solution containing the test compounds is washed from the wells. Binding of a test compound to a serine/threonine kinase polypeptide is detected by fluorescence measurements of the contents of the wells. A test compound that increases the fluorescence in a well by at least 15% relative to fluorescence of a well in which a test compound is not incubated is identified as a compound which binds to a serine/threonine kinase polypeptide.

EXAMPLE 4

Identification of a test compound which decreases serine/threonine kinase gene expression

A test compound is administered to a culture of human cells transfected with a serine/threonine kinase expression construct and incubated at 37 °C for 10 to 45 minutes. A culture of the same type of cells that have not been transfected is incubated for the same time without the test compound to provide a negative control. RNA is isolated from the two cultures as described in Chirgwin *et al.*, *Biochem. 18*, 5294-99, 1979). Northern blots are prepared using 20 to 30 µg total RNA and hybridized with a ^{32}P-labeled serine/threonine kinase-specific probe at 65°C in Express-hyb (CLONTECH). The probe comprises at least 11 contiguous nucleotides selected from the complement of SEQ ID NO:1 or 4. A test compound that decreases the serine/threonine kinase-specific signal relative to the signal obtained in the absence of the test compound is identified as an inhibitor of serine/threonine kinase gene expression.

EXAMPLE 5

Identification of a test compound which decreases serine/threonine kinase activity

A test compound is administered to a culture of human cells transfected with a serine/threonine kinase expression construct and incubated at 37°C for 10 to 45 minutes. A culture of the same type of cells that have not been transfected is incubated for the same time without the test compound to provide a negative control. serine/threonine kinase activity is measured using the method of in Trost *et al.*, *J. Biol. Chem. 275*, 7373-77, 2000; Hayashi *et al.*, *Biochem. Biophys. Res. Commun. 264*, 449-56, 1999; Masure *et al.*, *Eur. J. Biochem. 265*, 353-60, 1999; and Mukhopadhyay *et al.*, *J. Bacteriol. 181*, 6615-22, 1999 .

A test compound which decreases the serine/threonine kinase activity of the serine/threonine kinase relative to the serine/threonine kinase activity in the absence of the test compound is identified as an inhibitor of serine/threonine kinase activity.

EXAMPLE 6

Tissue-specific expression of serine/threonine kinase

The qualitative expression pattern of serine/threonine kinase in various tissues is determined by Reverse Transcription-Polymerase Chain Reaction (RT-PCR).

To demonstrate that human serine/threonine kinase is involved in cancer, expression is determined in the following tissues: adrenal gland, bone marrow, brain, cerebellum, colon, fetal brain, fetal liver, heart, kidney, liver, lung, mammary gland, pancreas, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thymus, thyroid, trachea, uterus, and peripheral blood lymphocytes. Expression in the following cancer cell lines also is determined: DU-145 (prostate), NCI-H125 (lung), HT-29 (colon), COLO-205 (colon), A-549 (lung), NCI-H460 (lung), HT-116 (colon), DLD-1 (colon), MDA-MD-231 (breast), LS174T (colon), ZF-75 (breast), MDA-MN-435 (breast), HT-1080, MCF-7 (breast), and U87. Matched pairs of malignant and normal tissue from the same patient also are tested.

To demonstrate that human serine/threonine kinase is involved in the disease process of diabetes, the following whole body panel is screened to show predominant or relatively high expression: subcutaneous and mesenteric adipose tissue, adrenal gland, bone marrow, brain, colon, fetal brain, heart, hypothalamus, kidney, liver, lung, mammary gland, pancreas, placenta, prostate, salivary gland, skeletal muscle, small intestine, spleen, stomach, testis, thymus, thyroid, trachea, and uterus. Human islet cells and an islet cell library also are tested. As a final step, the expression of human serine/threonine kinase in cells derived from normal individuals with the expression of cells derived from diabetic individuals is compared.

To demonstrate that human serine/threonine kinase is involved in CNS disorders, the following tissues are screened: fetal and adult brain, muscle, heart, lung, kidney, liver, thymus, testis, colon, placenta, trachea, pancreas, kidney, gastric mucosa, colon, liver, cerebellum, skin, cortex (Alzheimer's and normal), hypothalamus, cortex, amygdala, cerebellum, hippocampus, choroid, plexus, thalamus, and spinal cord.

To demonstrate that human serine/threonine kinase is involved in the disease process of COPD, the initial expression panel consists of RNA samples from respiratory tissues and inflammatory cells relevant to COPD: lung (adult and fetal), trachea, freshly isolated alveolar type II cells, cultured human bronchial epithelial cells, cultured small airway epithelial cells, cultured bronchial sooth muscle cells, cultured H441 cells (Clara-like), freshly isolated neutrophils and monocytes, and cultured monocytes (macrophage-like). Body map profiling also is carried out, using total RNA panels purchased from Clontech. The tissues are adrenal gland, bone marrow, brain, colon, heart, kidney, liver, lung, mammary gland, pancreas, prostate, salivary gland, skeletal muscle, small intestine, spleen, stomach, testis, thymus, trachea, thyroid, and uterus.

Quantitative expression profiling. Quantitative expression profiling is performed by the form of quantitative PCR analysis called "kinetic analysis" firstly described in Higuchi *et al.*, *BioTechnology 10*, 413-17, 1992, and Higuchi *et al.*, *BioTechnology 11*, 1026-30, 1993. The principle is that at any given cycle within the exponential phase of PCR, the amount of product is proportional to the initial number of template copies.

If the amplification is performed in the presence of an internally quenched fluorescent oligonucleotide (TaqMan probe) complementary to the target sequence, the probe is cleaved by the 5'-3' endonuclease activity of Taq DNA polymerase and a fluorescent dye released in the medium (Holland *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 88*, 7276-80, 1991). Because the fluorescence emission will increase in direct

proportion to the amount of the specific amplified product, the exponential growth phase of PCR product can be detected and used to determine the initial template concentration (Heid *et al.*, *Genome Res. 6*, 986-94, 1996, and Gibson *et al.*, *Genome Res. 6*, 995-1001, 1996).

The amplification of an endogenous control can be performed to standardize the amount of sample RNA added to a reaction. In this kind of experiment, the control of choice is the 18S ribosomal RNA. Because reporter dyes with differing emission spectra are available, the target and the endogenous control can be independently quantified in the same tube if probes labeled with different dyes are used.

All "real time PCR" measurements of fluorescence are made in the ABI Prism 7700.

RNA extraction and cDNA preparation. Total RNA from the tissues listed above are used for expression quantification. RNAs labeled "from autopsy" were extracted from autoptic tissues with the TRIzol reagent (Life Technologies, MD) according to the manufacturer's protocol.

Fifty µg of each RNA were treated with DNase I for 1 hour at 37°C in the following reaction mix: 0.2 U/µl RNase-free DNase I (Roche Diagnostics, Germany); 0.4 U/µl RNase inhibitor (PE Applied Biosystems, CA); 10 mM Tris-HCl pH 7.9; 10mM $MgCl_2$; 50 mM NaCl; and 1 mM DTT.

After incubation, RNA is extracted once with 1 volume of phenol:chloroform:isoamyl alcohol (24:24:1) and once with chloroform, and precipitated with 1/10 volume of 3 M sodium acetate, pH5.2, and 2 volumes of ethanol.

Fifty µg of each RNA from the autoptic tissues are DNase treated with the DNA-free kit purchased from Ambion (Ambion, TX). After resuspension and spectrophotometric quantification, each sample is reverse transcribed with the TaqMan Reverse Transcription Reagents (PE Applied Biosystems, CA) according to the manu-

facturer's protocol. The final concentration of RNA in the reaction mix is 200ng/μL. Reverse transcription is carried out with 2.5μM of random hexamer primers.

TaqMan quantitative analysis. Specific primers and probe are designed according to the recommendations of PE Applied Biosystems; the probe can be labeled at the 5' end FAM (6-carboxy-fluorescein) and at the 3' end with TAMRA (6-carboxy-tetramethyl-rhodamine). Quantification experiments are performed on 10 ng of reverse transcribed RNA from each sample. Each determination is done in triplicate.

Total cDNA content is normalized with the simultaneous quantification (multiplex PCR) of the 18S ribosomal RNA using the Pre-Developed TaqMan Assay Reagents (PDAR) Control Kit (PE Applied Biosystems, CA).

The assay reaction mix is as follows: 1X final TaqMan Universal PCR Master Mix (from 2X stock) (PE Applied Biosystems, CA); 1X PDAR control – 18S RNA (from 20X stock); 300 nM forward primer; 900 nM reverse primer; 200 nM probe; 10 ng cDNA; and water to 25 μl.

Each of the following steps are carried out once: pre PCR, 2 minutes at 50° C, and 10 minutes at 95°C. The following steps are carried out 40 times: denaturation, 15 seconds at 95°C, annealing/extension, 1 minute at 60°C.

The experiment is performed on an ABI Prism 7700 Sequence Detector (PE Applied Biosystems, CA). At the end of the run, fluorescence data acquired during PCR are processed as described in the ABI Prism 7700 user's manual in order to achieve better background subtraction as well as signal linearity with the starting target quantity.

EXAMPLE 7

Proliferation inhibition assay: Antisense oligonucleotides suppress the growth of cancer cell lines

The cell line used for testing is the human colon cancer cell line HCT116. Cells are cultured in RPMI-1640 with 10-15% fetal calf serum at a concentration of 10;000 cells per milliliter in a volume of 0.5 ml and kept at 37 °C in a 95% air/5%CO_2 atmosphere.

Phosphorothioate oligoribonucleotides are synthesized on an Applied Biosystems Model 380B DNA synthesizer using phosphoroamidite chemistry. A sequence of 24 bases complementary to the nucleotides at position 1 to 24 of SEQ ID NO:1 is used as the test oligonucleotide. As a control, another (random) sequence is used: 5'-TCA ACT GAC TAG ATG TAC ATG GAC-3'. Following assembly and deprotection, oligonucleotides are ethanol-precipitated twice, dried, and suspended in phosphate buffered saline at the desired concentration. Purity of the oligonucleotides is tested by capillary gel electrophoresis and ion exchange HPLC. The purified oligonucleotides are added to the culture medium at a concentration of 10 µM once per day for seven days.

The addition of the test oligonucleotide for seven days results in significantly reduced expression of human serine/threonine kinase as determined by Western blotting. This effect is not observed with the control oligonucleotide. After 3 to 7 days, the number of cells in the cultures is counted using an automatic cell counter. The number of cells in cultures treated with the test oligonucleotide (expressed as 100%) is compared with the number of cells in cultures treated with the control oligonucleotide. The number of cells in cultures treated with the test oligonucleotide is not more than 30% of control, indicating that the inhibition of human serine/threonine kinase has an anti-proliferative effect on cancer cells.

EXAMPLE 8

In vivo testing of compounds/target validation

1. Acute Mechanistic Assays

1.1. Reduction in Mitogenic Plasma Hormone Levels

This non-tumor assay measures the ability of a compound to reduce either the endogenous level of a circulating hormone or the level of hormone produced in response to a biologic stimulus. Rodents are administered test compound (p.o., i.p., i.v., i.m., or s.c.). At a predetermined time after administration of test compound, blood plasma is collected. Plasma is assayed for levels of the hormone of interest. If the normal circulating levels of the hormone are too low and/or variable to provide consistent results, the level of the hormone may be elevated by a pre-treatment with a biologic stimulus (i.e., LHRH may be injected i.m. into mice at a dosage of 30 ng/mouse to induce a burst of testosterone synthesis). The timing of plasma collection would be adjusted to coincide with the peak of the induced hormone response. Compound effects are compared to a vehicle-treated control group. An F-test is preformed to determine if the variance is equal or unequal followed by a Student's t-test. Significance is p value $\leq$ 0.05 compared to the vehicle control group.

1.2. Hollow Fiber Mechanism of Action Assay

Hollow fibers are prepared with desired cell line(s) and implanted intraperitoneally and/or subcutaneously in rodents. Compounds are administered p.o., i.p., i.v., i.m., or s.c. Fibers are harvested in accordance with specific readout assay protocol, these may include assays for gene expression (bDNA, PCR, or Taqman), or a specific biochemical activity (i.e., cAMP levels. Results are analyzed by Student's t-test or Rank Sum test after the variance between groups is compared by an F-test, with significance at $p \leq 0.05$ as compared to the vehicle control group.

2. Subacute Functional *In Vivo* Assays

2.1. Reduction in Mass of Hormone Dependent Tissues

This is another non-tumor assay that measures the ability of a compound to reduce the mass of a hormone dependent tissue (i.e., seminal vesicles in males and uteri in females). Rodents are administered test compound (p.o., i.p., i.v., i.m., or s.c.) according to a predetermined schedule and for a predetermined duration (i.e., 1 week). At termination of the study, animals are weighed, the target organ is excised, any fluid is expressed, and the weight of the organ is recorded. Blood plasma may also be collected. Plasma may be assayed for levels of a hormone of interest or for levels of test agent. Organ weights may be directly compared or they may be normalized for the body weight of the animal. Compound effects are compared to a vehicle-treated control group. An F-test is preformed to determine if the variance is equal or unequal followed by a Student's t-test. Significance is p value $\leq$ 0.05 compared to the vehicle control group.

2.2. Hollow Fiber Proliferation Assay

Hollow fibers are prepared with desired cell line(s) and implanted intraperitoneally and/or subcutaneously in rodents. Compounds are administered p.o., i.p., i.v., i.m., or s.c. Fibers are harvested in accordance with specific readout assay protocol. Cell proliferation is determined by measuring a marker of cell number (i.e., MTT or LDH). The cell number and change in cell number from the starting inoculum are analyzed by Student's t-test or Rank Sum test after the variance between groups is compared by an F-test, with significance at $p \leq 0.05$ as compared to the vehicle control group.

2.3. Anti-angiogenesis Models

2.3.1. Corneal Angiogenesis

Hydron pellets with or without growth factors or cells are implanted into a micropocket surgically created in the rodent cornea. Compound administration may be systemic or local (compound mixed with growth factors in the hydron pellet). Corneas are harvested at 7 days post implantation immediately following intracardiac infusion of colloidal carbon and are fixed in 10% formalin. Readout is qualitative scoring and/or image analysis. Qualitative scores are compared by Rank Sum test. Image analysis data is evaluated by measuring the area of neovascularization (in pixels) and group averages are compared by Student's t-test (2 tail). Significance is $p \leq 0.05$ as compared to the growth factor or cells only group.

2.3.2. Matrigel Angiogenesis

Matrigel, containing cells or growth factors, is injected subcutaneously. Compounds are administered p.o., i.p., i.v., i.m., or s.c. Matrigel plugs are harvested at predetermined time point(s) and prepared for readout. Readout is an ELISA-based assay for hemoglobin concentration and/or histological examination (i.e. vessel count, special staining for endothelial surface markers: CD31, factor-8). Readouts are analyzed by Student's t-test, after the variance between groups is compared by an F-test, with significance determined at $p \leq 0.05$ as compared to the vehicle control group.

3. Primary Antitumor Efficacy

3.1. Early Therapy Models

3.1.1. Subcutaneous Tumor

Tumor cells or fragments are implanted subcutaneously on Day 0. Vehicle and/or compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule starting at a time, usually on Day 1, prior to the ability to measure the tumor burden. Body weights and tumor measurements are recorded 2-3 times weekly. Mean net body and tumor weights are calculated for each data collection day. Anti-tumor efficacy may be initially determined by comparing the size of treated (T) and control (C) tumors on a given day by a Student's t-test, after the variance between groups is compared by an F-test, with significance determined at $p \leq 0.05$. The experiment may also be continued past the end of dosing in which case tumor measurements would continue to be recorded to monitor tumor growth delay. Tumor growth delays are expressed as the difference in the median time for the treated and control groups to attain a predetermined size divided by the median time for the control group to attain that size. Growth delays are compared by generating Kaplan-Meier curves from the times for individual tumors to attain the evaluation size. Significance is $p \leq 0.05$.

3.1.2. Intraperitoneal/Intracranial Tumor Models

Tumor cells are injected intraperitoneally or intracranially on Day 0. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule starting on Day 1. Observations of morbidity and/or mortality are recorded twice daily. Body weights are measured and recorded twice weekly. Morbidity/mortality data is expressed in terms of the median time of survival and the number of long-term survivors is indicated separately. Survival times are used to generate Kaplan-

Meier curves. Significance is $p \leq 0.05$ by a log-rank test compared to the control group in the experiment.

3.2. Established Disease Model

Tumor cells or fragments are implanted subcutaneously and grown to the desired size for treatment to begin. Once at the predetermined size range, mice are randomized into treatment groups. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule. Tumor and body weights are measured and recorded 2-3 times weekly. Mean tumor weights of all groups over days post inoculation are graphed for comparison. An F-test is preformed to determine if the variance is equal or unequal followed by a Student's t-test to compare tumor sizes in the treated and control groups at the end of treatment. Significance is $p \leq 0.05$ as compared to the control group. Tumor measurements may be recorded after dosing has stopped to monitor tumor growth delay. Tumor growth delays are expressed as the difference in the median time for the treated and control groups to attain a predetermined size divided by the median time for the control group to attain that size. Growth delays are compared by generating Kaplan-Meier curves from the times for individual tumors to attain the evaluation size. Significance is p value$\leq$ 0.05 compared to the vehicle control group.

3.3. Orthotopic Disease Models

3.3.1. Mammary Fat Pad Assay

Tumor cells or fragments, of mammary adenocarcinoma origin, are implanted directly into a surgically exposed and reflected mammary fat pad in rodents. The fat pad is placed back in its original position and the surgical site is closed. Hormones may also be administered to the rodents to support the growth of the tumors. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined

schedule. Tumor and body weights are measured and recorded 2-3 times weekly. Mean tumor weights of all groups over days post inoculation are graphed for comparison. An F-test is preformed to determine if the variance is equal or unequal followed by a Student's t-test to compare tumor sizes in the treated and control groups at the end of treatment. Significance is $p \leq 0.05$ as compared to the control group.

Tumor measurements may be recorded after dosing has stopped to monitor tumor growth delay. Tumor growth delays are expressed as the difference in the median time for the treated and control groups to attain a predetermined size divided by the median time for the control group to attain that size. Growth delays are compared by generating Kaplan-Meier curves from the times for individual tumors to attain the evaluation size. Significance is p value≤ 0.05 compared to the vehicle control group. In addition, this model provides an opportunity to increase the rate of spontaneous metastasis of this type of tumor. Metastasis can be assessed at termination of the study by counting the number of visible foci per target organ, or measuring the target organ weight. The means of these endpoints are compared by Student's t-test after conducting an F-test, with significance determined at $p \leq 0.05$ compared to the control group in the experiment.

3.3.2. Intraprostatic Assay

Tumor cells or fragments, of prostatic adenocarcinoma origin, are implanted directly into a surgically exposed dorsal lobe of the prostate in rodents. The prostate is externalized through an abdominal incision so that the tumor can be implanted specifically in the dorsal lobe while verifying that the implant does not enter the seminal vesicles. The successfully inoculated prostate is replaced in the abdomen and the incisions through the abdomen and skin are closed. Hormones may also be administered to the rodents to support the growth of the tumors. Compounds are

administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule. Body weights are measured and recorded 2-3 times weekly. At a predetermined time, the experiment is terminated and the animal is dissected. The size of the primary tumor is measured in three dimensions using either a caliper or an ocular micrometer attached to a dissecting scope. An F-test is preformed to determine if the variance is equal or unequal followed by a Student's t-test to compare tumor sizes in the treated and control groups at the end of treatment. Significance is $p \leq 0.05$ as compared to the control group. This model provides an opportunity to increase the rate of spontaneous metastasis of this type of tumor. Metastasis can be assessed at termination of the study by counting the number of visible foci per target organ (i.e., the lungs), or measuring the target organ weight (i.e., the regional lymph nodes). The means of these endpoints are compared by Student's t-test after conducting an F-test, with significance determined at $p \leq 0.05$ compared to the control group in the experiment.

3.3.3. Intrabronchial Assay

Tumor cells of pulmonary origin may be implanted intrabronchially by making an incision through the skin and exposing the trachea. The trachea is pierced with the beveled end of a 25 gauge needle and the tumor cells are inoculated into the main bronchus using a flat-ended 27 gauge needle with a 90° bend. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule. Body weights are measured and recorded 2-3 times weekly. At a predetermined time, the experiment is terminated and the animal is dissected. The size of the primary tumor is measured in three dimensions using either a caliper or an ocular micrometer attached to a dissecting scope. An F-test is preformed to determine if the variance is equal or unequal followed by a Student's t-test to compare tumor sizes in the treated and control groups at the end of treatment. Significance is $p \leq 0.05$ as compared to the control group. This model provides an opportunity to increase the rate of spontaneous metastasis of this type of tumor. Metastasis can be assessed at ter-

mination of the study by counting the number of visible foci per target organ (i.e., the contralateral lung), or measuring the target organ weight. The means of these endpoints are compared by Student's t-test after conducting an F-test, with significance determined at $p \leq 0.05$ compared to the control group in the experiment.

3.3.4. Intracecal Assay

Tumor cells of gastrointestinal origin may be implanted intracecally by making an abdominal incision through the skin and externalizing the intestine. Tumor cells are inoculated into the cecal wall without penetrating the lumen of the intestine using a 27 or 30 gauge needle. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule. Body weights are measured and recorded 2-3 times weekly. At a predetermined time, the experiment is terminated and the animal is dissected. The size of the primary tumor is measured in three dimensions using either a caliper or an ocular micrometer attached to a dissecting scope. An F-test is preformed to determine if the variance is equal or unequal followed by a Student's t-test to compare tumor sizes in the treated and control groups at the end of treatment. Significance is $p \leq 0.05$ as compared to the control group. This model provides an opportunity to increase the rate of spontaneous metastasis of this type of tumor. Metastasis can be assessed at termination of the study by counting the number of visible foci per target organ (i.e., the liver), or measuring the target organ weight. The means of these endpoints are compared by Student's t-test after conducting an F-test, with significance determined at $p \leq 0.05$ compared to the control group in the experiment.

4. Secondary (Metastatic) Antitumor Efficacy

4.1. Spontaneous Metastasis

Tumor cells are inoculated s.c. and the tumors allowed to grow to a predetermined range for spontaneous metastasis studies to the lung or liver. These primary tumors are then excised. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule which may include the period leading up to the excision of the primary tumor to evaluate therapies directed at inhibiting the early stages of tumor metastasis. Observations of morbidity and/or mortality are recorded daily. Body weights are measured and recorded twice weekly. Potential endpoints include survival time, numbers of visible foci per target organ, or target organ weight. When survival time is used as the endpoint the other values are not determined. Survival data is used to generate Kaplan-Meier curves. Significance is $p \leq 0.05$ by a log-rank test compared to the control group in the experiment. The mean number of visible tumor foci, as determined under a dissecting microscope, and the mean target organ weights are compared by Student's t-test after conducting an F-test, with significance determined at $p \leq 0.05$ compared to the control group in the experiment for both of these endpoints.

4.2. Forced Metastasis

Tumor cells are injected into the tail vein, portal vein, or the left ventricle of the heart in experimental (forced) lung, liver, and bone metastasis studies, respectively. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule. Observations of morbidity and/or mortality are recorded daily. Body weights are measured and recorded twice weekly. Potential endpoints include survival time, numbers of visible foci per target organ, or target organ weight. When survival time is used as the endpoint the other values are not determined. Survival data is used to generate Kaplan-Meier curves. Significance is $p \leq 0.05$ by a log-rank

test compared to the control group in the experiment. The mean number of visible tumor foci, as determined under a dissecting microscope, and the mean target organ weights are compared by Student's t-test after conducting an F-test, with significance at $p \leq 0.05$ compared to the vehicle control group in the experiment for both endpoints.

EXAMPLE 9

Diabetes: In vivo testing of compounds/target validation

1. Glucose Production:

Over-production of glucose by the liver, due to an enhanced rate of gluconeogenesis, is the major cause of fasting hyperglycemia in diabetes. Overnight fasted normal rats or mice have elevated rates of gluconeogenesis as do streptozotocin-induced diabetic rats or mice fed ad libitum. Rats are made diabetic with a single intravenous injection of 40 mg/kg of streptozotocin while C57BL/KsJ mice are given 40-60 mg/kg i.p. for 5 consecutive days. Blood glucose is measured from tail-tip blood and then compounds are administered via different routes (p.o., i.p., i.v., s.c.). Blood is collected at various times thereafter and glucose measured. Alternatively, compounds are administered for several days, then the animals are fasted overnight, blood is collected and plasma glucose measured. Compounds that inhibit glucose production will decrease plasma glucose levels compared to the vehicle-treated control group.

2. Insulin Sensitivity:

Both ob/ob and db/db mice as well as diabetic Zucker rats are hyperglycemic, hyperinsulinemic and insulin resistant. The animals are pre-bled, their glucose levels measured, and then they are grouped so that the mean glucose level is the same for each group. Compounds are administered daily either q.d. or b.i.d. by different

routes (p.o., i.p., s.c.) for 7-28 days. Blood is collected at various times and plasma glucose and insulin levels determined. Compounds that improve insulin sensitivity in these models will decrease both plasma glucose and insulin levels when compared to the vehicle-treated control group.

3. Insulin Secretion:

Compounds that enhance insulin secretion from the pancreas will increase plasma insulin levels and improve the disappearance of plasma glucose following the administration of a glucose load. When measuring insulin levels, compounds are administered by different routes (p.o., i.p., s.c. or i.v.) to overnight fasted normal rats or mice. At the appropriate time an intravenous glucose load (0.4g/kg) is given, blood is collected one minute later. Plasma insulin levels are determined. Compounds that enhance insulin secretion will increase plasma insulin levels compared to animals given only glucose. When measuring glucose disappearance, animals are bled at the appropriate time after compound administration, then given either an oral or intraperitoneal glucose load (1g/kg), bled again after 15, 30, 60 and 90 minutes and plasma glucose levels determined. Compounds that increase insulin levels will decrease glucose levels and the area-under-the glucose curve when compared to the vehicle-treated group given only glucose.

EXAMPLE 10

In vivo testing of compounds/target validation

1. Pain:

Acute Pain

Acute pain is measured on a hot plate mainly in rats. Two variants of hot plate testing are used: In the classical variant animals are put on a hot surface (52 to 56 °C) and the latency time is measured until the animals show nocifensive behavior, such as stepping or foot licking. The other variant is an increasing temperature hot plate

where the experimental animals are put on a surface of neutral temperature. Subsequently this surface is slowly but constantly heated until the animals begin to lick a hind paw. The temperature which is reached when hind paw licking begins is a measure for pain threshold.

Compounds are tested against a vehicle treated control group. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.

Persistent Pain

Persistent pain is measured with the formalin or capsaicin test, mainly in rats. A solution of 1 to 5% formalin or 10 to 100 µg capsaicin is injected into one hind paw of the experimental animal. After formalin or capsaicin application the animals show nocifensive reactions like flinching, licking and biting of the affected paw. The number of nocifensive reactions within a time frame of up to 90 minutes is a measure for intensity of pain.

Compounds are tested against a vehicle treated control group. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to formalin or capsaicin administration.

Neuropathic Pain

Neuropathic pain is induced by different variants of unilateral sciatic nerve injury mainly in rats. The operation is performed under anesthesia. The first variant of sciatic nerve injury is produced by placing loosely constrictive ligatures around the common sciatic nerve. The second variant is the tight ligation of about the half of the

diameter of the common sciatic nerve. In the next variant, a group of models is used in which tight ligations or transections are made of either the L5 and L6 spinal nerves, or the L% spinal nerve only. The fourth variant involves an axotomy of two of the three terminal branches of the sciatic nerve (tibial and common peroneal nerves) leaving the remaining sural nerve intact whereas the last variant comprises the axotomy of only the tibial branch leaving the sural and common nerves uninjured. Control animals are treated with a sham operation.

Postoperatively, the nerve injured animals develop a chronic mechanical allodynia, cold allodynioa, as well as a thermal hyperalgesia. Mechanical allodynia is measured by means of a pressure transducer (electronic von Frey Anesthesiometer, IITC Inc.-Life Science Instruments, Woodland Hills, SA, USA; Electronic von Frey System, Somedic Sales AB, Hörby, Sweden). Thermal hyperalgesia is measured by means of a radiant heat source (Plantar Test, Ugo Basile, Comerio, Italy), or by means of a cold plate of 5 to 10 °C where the nocifensive reactions of the affected hind paw are counted as a measure of pain intensity. A further test for cold induced pain is the counting of nocifensive reactions, or duration of nocifensive responses after plantar administration of acetone to the affected hind limb. Chronic pain in general is assessed by registering the circadanian rhythms in activity (Surjo and Arndt, Universität zu Köln, Cologne, Germany), and by scoring differences in gait (foot print patterns; FOOTPRINTS program, Klapdor et al., 1997. A low cost method to analyze footprint patterns. J. Neurosci. Methods 75, 49-54).

Compounds are tested against sham operated and vehicle treated control groups. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.

Inflammatory Pain

Inflammatory pain is induced mainly in rats by injection of 0.75 mg carrageenan or complete Freund's adjuvant into one hind paw. The animals develop an edema with mechanical allodynia as well as thermal hyperalgesia. Mechanical allodynia is measured by means of a pressure transducer (electronic von Frey Anesthesiometer, IITC Inc.-Life Science Instruments, Woodland Hills, SA, USA). Thermal hyperalgesia is measured by means of a radiant heat source (Plantar Test, Ugo Basile, Comerio, Italy, Paw thermal stimulator, G. Ozaki, University of California, USA). For edema measurement two methods are being used. In the first method, the animals are sacrificed and the affected hindpaws sectioned and weighed. The second method comprises differences in paw volume by measuring water displacement in a plethysmometer (Ugo Basile, Comerio, Italy).

Compounds are tested against uninflamed as well as vehicle treated control groups. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.

Diabetic Neuropathic Pain

Rats treated with a single intraperitoneal injection of 50 to 80 mg/kg streptozotocin develop a profound hyperglycemia and mechanical allodynia within 1 to 3 weeks. Mechanical allodynia is measured by means of a pressure transducer (electronic von Frey Anesthesiometer, IITC Inc.-Life Science Instruments, Woodland Hills, SA, USA).

Compounds are tested against diabetic and non-diabetic vehicle treated control groups. Substance application is performed at different time points via different

application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.

2. Parkinson's disease

6-Hydroxydopamine (6-OH-DA) Lesion

Degeneration of the dopaminergic nigrostriatal and striatopallidal pathways is the central pathological event in Parkinson's disease. This disorder has been mimicked experimentally in rats using single/sequential unilateral stereotaxic injections of 6-OH-DA into the medium forebrain bundle (MFB).

Male Wistar rats (Harlan Winkelmann, Germany), weighing 200±250 g at the beginning of the experiment, are used. The rats are maintained in a temperature- and humidity-controlled environment under a 12 h light/dark cycle with free access to food and water when not in experimental sessions. The following in vivo protocols are approved by the governmental authorities. All efforts are made to minimize animal suffering, to reduce the number of animals used, and to utilize alternatives to in vivo techniques.

Animals are administered pargyline on the day of surgery (Sigma, St. Louis, MO, USA; 50 mg/kg i.p.) in order to inhibit metabolism of 6-OHDA by monoamine oxidase and desmethylimipramine HCl (Sigma; 25 mg/kg i.p.) in order to prevent uptake of 6-OHDA by noradrenergic terminals. Thirty minutes later the rats are anesthetized with sodium pentobarbital (50 mg/kg) and placed in a stereotaxic frame. In order to lesion the DA nigrostriatal pathway 4 µl of 0.01% ascorbic acid-saline containing 8 µg of 6-OHDA HBr (Sigma) are injected into the left medial fore-brain bundle at a rate of 1 µl/min (2.4 mm anterior, 1.49 mm lateral, -2.7 mm ventral to

Bregma and the skull surface). The needle is left in place an additional 5 min to allow diffusion to occur.

Stepping Test

Forelimb akinesia is assessed three weeks following lesion placement using a modified stepping test protocol. In brief, the animals are held by the experimenter with one hand fixing the hindlimbs and slightly raising the hind part above the surface. One paw is touching the table, and is then moved slowly sideways (5 s for 1 m), first in the forehand and then in the backhand direction. The number of adjusting steps is counted for both paws in the backhand and forehand direction of movement. The sequence of testing is right paw forehand and backhand adjusting stepping, followed by left paw forehand and backhand directions. The test is repeated three times on three consecutive days, after an initial training period of three days prior to the first testing. Forehand adjusted stepping reveals no consistent differences between lesioned and healthy control animals. Analysis is therefore restricted to backhand adjusted stepping.

Balance Test

Balance adjustments following postural challenge are also measured during the stepping test sessions. The rats are held in the same position as described in the stepping test and, instead of being moved sideways, tilted by the experimenter towards the side of the paw touching the table. This maneuver results in loss of balance and the ability of the rats to regain balance by forelimb movements is scored on a scale ranging from 0 to 3. Score 0 is given for a normal forelimb placement. When the forelimb movement is delayed but recovery of postural balance detected, score 1 is given. Score 2 represents a clear, yet insufficient, forelimb reaction, as evidenced by muscle contraction, but lack of success in recovering balance, and score

3 is given for no reaction of movement. The test is repeated three times a day on each side for three consecutive days after an initial training period of three days prior to the first testing.

Staircase Test (Paw Reaching)

A modified version of the staircase test is used for evaluation of paw reaching behavior three weeks following primary and secondary lesion placement. Plexiglass test boxes with a central platform and a removable staircase on each side are used. The apparatus is designed such that only the paw on the same side at each staircase can be used, thus providing a measure of independent forelimb use. For each test the animals are left in the test boxes for 15 min. The double staircase is filled with 7 x 3 chow pellets (Precision food pellets, formula: P, purified rodent diet, size 45 mg; Sandown Scientific) on each side. After each test the number of pellets eaten (successfully retrieved pellets) and the number of pellets taken (touched but dropped) for each paw and the success rate (pellets eaten/pellets taken) are counted separately. After three days of food deprivation (12 g per animal per day) the animals are tested for 11 days. Full analysis is conducted only for the last five days.

MPTP treatment

The neurotoxin 1-methyl-4-phenyl-1,2,3,6-tetrahydro-pyridine (MPTP) causes degeneration of mesencephalic dopaminergic (DAergic) neurons in rodents, non-human primates, and humans and, in so doing, reproduces many of the symptoms of Parkinson's disease. MPTP leads to a marked decrease in the levels of dopamine and its metabolites, and in the number of dopaminergic terminals in the striatum as well as severe loss of the tyrosine hydroxylase (TH)-immunoreactive cell bodies in the substantia nigra, pars compacta.

In order to obtain severe and long-lasting lesions, and to reduce mortality, animals receive single injections of MPTP, and are then tested for severity of lesion 7–10 days later. Successive MPTP injections are administered on days 1, 2 and 3. Animals receive application of 4 mg/kg MPTP hydrochloride (Sigma) in saline once daily. All injections are intraperitoneal (i.p.) and the MPTP stock solution is frozen between injections. Animals are decapitated on day 11.

Immunohistology

At the completion of behavioral experiments, all animals are anaesthetized with 3 ml thiopental (1 g/40 ml i.p., Tyrol Pharma). The mice are perfused transcardially with 0.01 M PBS (pH 7.4) for 2 min, followed by 4% paraformaldehyde (Merck) in PBS for 15 min. The brains are removed and placed in 4% paraformaldehyde for 24 h at 4 °C. For dehydration they are then transferred to a 20% sucrose (Merck) solution in 0.1 M PBS at 4 °C until they sink. The brains are frozen in methylbutan at -20 °C for 2 min and stored at -70 °C. Using a sledge microtome (mod. 3800-Frigocut, Leica), 25 µm sections are taken from the genu of the corpus callosum (AP 1.7 mm) to the hippocampus (AP 21.8 mm) and from AP 24.16 to AP 26.72. Forty-six sections are cut and stored in assorters in 0.25 M Tris buffer (pH 7.4) for immunohistochemistry.

A series of sections is processed for free-floating tyrosine hydroxylase (TH) immunohistochemistry. Following three rinses in 0.1 M PBS, endogenous peroxidase activity is quenched for 10 min in 0.3% H_2O_2 ±PBS. After rinsing in PBS, sections are preincubated in 10% normal bovine serum (Sigma) for 5 min as blocking agent and transferred to either primary anti-rat TH rabbit antiserum (dilution 1:2000).

Following overnight incubation at room temperature, sections for TH immunoreactivity are rinsed in PBS (2 x10 min) and incubated in biotinylated

anti-rabbit immunoglobulin G raised in goat (dilution 1:200) (Vector) for 90 min, rinsed repeatedly and transferred to Vectastain ABC (Vector) solution for 1 h. 3,.3' -Diaminobenzidine tetrahydrochloride (DAB; Sigma) in 0.1 M PBS, supplemented with 0.005% H_2O_2 , serves as chromogen in the subsequent visualization reaction. Sections are mounted on to gelatin-coated slides, left to dry overnight, counter-stained with hematoxylin dehydrated in ascending alcohol concentrations and cleared in butylacetate. Coverslips are mounted on entellan.

Rotarod Test

We use a modification of the procedure described by Rozas and Labandeira-Garcia (1997), with a CR-1 Rotamex system (Columbus Instruments, Columbus, OH) comprising an IBM-compatible personal computer, a CIO-24 data acquisition card, a control unit, and a four-lane rotarod unit. The rotarod unit consists of a rotating spindle (diameter 7.3 cm) and individual compartments for each mouse. The system software allows preprogramming of session protocols with varying rotational speeds (0–80 rpm). Infrared beams are used to detect when a mouse has fallen onto the base grid beneath the rotarod. The system logs the fall as the end of the experiment for that mouse, and the total time on the rotarod, as well as the time of the fall and all the set-up parameters, are recorded. The system also allows a weak current to be passed through the base grid, to aid training.

3. Dementia

The object recognition task

The object recognition task has been designed to assess the effects of experimental manipulations on the cognitive performance of rodents. A rat is placed in an open field, in which two identical objects are present. The rats inspects both objects during

the first trial of the object recognition task. In a second trial, after a retention interval of for example 24 hours, one of the two objects used in the first trial, the 'familiar' object, and a novel object are placed in the open field. The inspection time at each of the objects is registered. The basic measures in the OR task is the time spent by a rat exploring the two object the second trial. Good retention is reflected by higher exploration times towards the novel than the 'familiar' object.

Administration of the putative cognition enhancer prior to the first trial predominantly allows assessment of the effects on acquisition, and eventually on consolidation processes. Administration of the testing compound after the first trial allows to assess the effects on consolidation processes, whereas administration before the second trial allows to measure effects on retrieval processes.

The passive avoidance task

The passive avoidance task assesses memory performance in rats and mice. The inhibitory avoidance apparatus consists of a two-compartment box with a light compartment and a dark compartment. The two compartments are separated by a guillotine door that can be operated by the experimenter. A threshold of 2 cm separates the two compartments when the guillotine door is raised. When the door is open, the illumination in the dark compartment is about 2 lux. The light intensity is about 500 lux at the center of the floor of the light compartment.

Two habituation sessions, one shock session, and a retention session are given, separated by inter-session intervals of 24 hours. In the habituation sessions and the retention session the rat is allowed to explore the apparatus for 300 sec. The rat is placed in the light compartment, facing the wall opposite to the guillotine door. After an accommodation period of 15 sec. the guillotine door is opened so that all parts of the apparatus can be visited freely. Rats normally avoid brightly lit areas and will enter the dark compartment within a few seconds.

In the shock session the guillotine door between the compartments is lowered as soon as the rat has entered the dark compartment with its four paws, and a scrambled 1 mA footshock is administered for 2 sec. The rat is removed from the apparatus and put back into its home cage. The procedure during the retention session is identical to that of the habituation sessions.

The step-through latency, that is the first latency of entering the dark compartment (in sec.) during the retention session is an index of the memory performance of the animal; the longer the latency to enter the dark compartment, the better the retention is. A testing compound in given half an hour before the shock session, together with 1 $mg*kg^{-1}$ scopolamine. Scopolamine impairs the memory performance during the retention session 24 hours later. If the test compound increases the enter latency compared with the scopolamine-treated controls, is likely to possess cognition enhancing potential.

The Morris water escape task

The Morris water escape task measures spatial orientation learning in rodents. It is a test system that has extensively been used to investigate the effects of putative therapeutic on the cognitive functions of rats and mice. The performance of an animal is assessed in a circular water tank with an escape platform that is submerged about 1 cm below the surface of the water. The escape platform is not visible for an animal swimming in the water tank. Abundant extra-maze cues are provided by the furniture in the room, including desks, computer equipment, a second water tank, the presence of the experimenter, and by a radio on a shelf that is playing softly.

The animals receive four trials during five daily acquisition sessions. A trial is started by placing an animal into the pool, facing the wall of the tank. Each of four starting positions in the quadrants north, east, south, and west is used once in a series of four

trials; their order is randomized. The escape platform is always in the same position. A trial is terminated as soon as the animal had climbs onto the escape platform or when 90 seconds have elapsed, whichever event occurs first. The animal is allowed to stay on the platform for 30 seconds. Then it is taken from the platform and the next trial is started. If an animal did not find the platform within 90 seconds it is put on the platform by the experimenter and is allowed to stay there for 30 seconds. After the fourth trial of the fifth daily session, an additional trial is given as a probe trial: the platform is removed, and the time the animal spends in the four quadrants is measured for 30 or 60 seconds. In the probe trial, all animals start from the same start position, opposite to the quadrant where the escape platform had been positioned during acquisition.

Four different measures are taken to evaluate the performance of an animal during acquisition training: escape latency, traveled distance, distance to platform, and swimming speed. The following measures are evaluated for the probe trial: time (s) in quadrants and traveled distance (cm) in the four quadrants. The probe trial provides additional information about how well an animal learned the position of the escape platform. If an animal spends more time and swims a longer distance in the quadrant where the platform had been positioned during the acquisition sessions than in any other quadrant, one concludes that the platform position has been learned well.

In order to assess the effects of putative cognition enhancing compounds, rats or mice with specific brain lesions which impair cognitive functions, or animals treated with compounds such as scopolamine or MK-801, which interfere with normal learning, or aged animals which suffer from cognitive deficits, are used.

The T-maze spontaneous alternation task

The T-maze spontaneous alternation task (TeMCAT) assesses the spatial memory performance in mice. The start arm and the two goal arms of the T-maze are

provided with guillotine doors which can be operated manually by the experimenter. A mouse is put into the start arm at the beginning of training. The guillotine door is closed. In the first trial, the 'forced trial', either the left or right goal arm is blocked by lowering the guillotine door. After the mouse has been released from the start arm, it will negotiate the maze, eventually enter the open goal arm, and return to the start position, where it will be confined for 5 seconds, by lowering the guillotine door. Then, the animal can choose freely between the left and right goal arm (all guillotine-doors opened) during 14 'free choice' trials. As soon a the mouse has entered one goal arm, the other one is closed. The mouse eventually returns to the start arm and is free to visit whichever go alarm it wants after having been confined to the start arm for 5 seconds. After completion of 14 free choice trials in one session, the animal is removed from the maze. During training, the animal is never handled.

The percent alternations out of 14 trials is calculated. This percentage and the total time needed to complete the first forced trial and the subsequent 14 free choice trials (in s) is analyzed. Cognitive deficits are usually induced by an injection of scopolamine, 30 min before the start of the training session. Scopolamine reduced the per-cent alternations to chance level, or below. A cognition enhancer, which is always administered before the training session, will at least partially, antagonize the scopolamine-induced reduction in the spontaneous alternation rate.

EXAMPLE 11

Treatment of COPD in an animal model

Guinea pigs are exposed on a single occasion to tobacco smoke for 50 minutes. Animals are sacrificed between 10 minutes and 24 hour following the end of the exposure and their lungs placed in RNAlater™. The lung tissue is homogenized and total RNA is extracted using a Qiagen RNeasy™ Maxi kit. Molecular Probes RiboGreen™ RNA quantitation method is used to quantify the amount of RNA in each sample. Total RNA is reverse transcribed and the resultant cDNA was used in a

real-time polymerase chain reaction (PCR). The cDNA is added to a solution containing the sense and anti-sense primers and the 6-carboxy-tetramethyl-rhodamine labeled probe of the serine/threonine kinase. Cyclophilin is used as the housekeeping gene. The expression of the serine/threonine kinase is measured using the TaqMan real-time PCR system that generates an amplification curve for each sample. From this curve a threshold cycle value is calculated: the fractional cycle number at which the amount of amplified target reaches a fixed threshold. A sample containing many copies of the serine/threonine kinase will reach this threshold earlier than a sample containing fewer copies. The threshold is set at 0.2 and the threshold cycle C_T is calculated from the amplification curve. The C_T value for the serine/threonine kinase is normalized using the C_T value for the housekeeping gene.

Expression of the serine/threonine kinase is increased by at least 1,5-fold between 10 minutes and 3 hours post tobacco smoke exposure compared to air exposed control animals.

Test compounds are evaluated as follows. Animals are pre-treated with a test compound between 5 minutes and 1 hour prior to the tobacco smoke exposure and they are then sacrificed up to 3 hours after the tobacco smoke exposure has been completed. Control animals are pre-treated with the vehicle of the test compound via the route of administration chosen for the test compound. A test compound that reduces the tobacco smoke induced upregulation of the serine/threonine kinase relative to the expression seen in vehicle treated tobacco smoke exposed animals is identified as an inhibitor of serine/threonine kinase expression.

CLAIMS

1. An isolated polynucleotide being selected from the group consisting of:

a. a polynucleotide encoding a serine/threonine kinase polypeptide comprising an amino acid sequence selected form the group consisting of:

i. amino acid sequences which are at least about 30% identical to the amino acid sequence shown in SEQ ID NO: 2;

ii. the amino acid sequence shown in SEQ ID NO: 2;

iii. amino acid sequences which are at least about 30% identical to the amino acid sequence shown in SEQ ID NO: 5; and

iv. the amino acid sequence shown in SEQ ID NO: 5.

b. a polynucleotide comprising the sequence of SEQ ID NOS: 1; 4 or 8;

c. a polynucleotide which hybridizes under stringent conditions to a polynucleotide specified in (a) and (b) and encodes a serine/threonine kinase polypeptide;

d. a polynucleotide the sequence of which deviates from the polynucleotide sequences specified in (a) to (c) due to the degeneration of the genetic code and encodes a serine/threonine kinase polypeptide; and

e. a polynucleotide which represents a fragment, derivative or allelic variation of a polynucleotide sequence specified in (a) to (d) and encodes a serine/threonine kinase polypeptide.

2. An expression vector containing any polynucleotide of claim 1.

3. A host cell containing the expression vector of claim 2.

4. A substantially purified serine/threonine kinase polypeptide encoded by a polynucleotide of claim 1.

5. A method for producing a serine/threonine kinase polypeptide, wherein the method comprises the following steps:

a. culturing the host cell of claim 3 under conditions suitable for the expression of the serine/threonine kinase polypeptide; and

b. recovering the serine/threonine kinase polypeptide from the host cell culture.

6. A method for detection of a polynucleotide encoding a serine/threonine kinase polypeptide in a biological sample comprising the following steps:

a. hybridizing any polynucleotide of claim 1 to a nucleic acid material of a biological sample, thereby forming a hybridization complex; and

b. detecting said hybridization complex.

7. The method of claim 6, wherein before hybridization, the nucleic acid material of the biological sample is amplified.

8. A method for the detection of a polynucleotide of claim 1 or a serine/threonine kinase polypeptide of claim 4 comprising the steps of:

a. contacting a biological sample with a reagent which specifically interacts with the polynucleotide or the serine/threonine kinase polypeptide and

b. detecting the interaction.

9. A diagnostic kit for conducting the method of any one of claims 6 to 8.

10. A method of screening for agents which decrease the activity of a serine/threonine kinase, comprising the steps of:

a. contacting a test compound with any serine/threonine kinase polypeptide encoded by any polynucleotide of claim1;

b. detecting binding of the test compound to the serine/threonine kinase polypeptide, wherein a test compound which binds to the polypeptide

is identified as a potential therapeutic agent for decreasing the activity of a serine/threonine kinase.

11. A method of screening for agents which regulate the activity of a serine/threonine kinase, comprising the steps of:

a. contacting a test compound with a serine/threonine kinase polypeptide encoded by any polynucleotide of claim 1; and

b. detecting a serine/threonine kinase activity of the polypeptide, wherein a test compound which increases the serine/threonine kinase activity is identified as a potential therapeutic agent for increasing the activity of the serine/threonine kinase, and wherein a test compound which decreases the serine/threonine kinase activity of the polypeptide is identified as a potential therapeutic agent for decreasing the activity of the serine/threonine kinase.

12. A method of screening for agents which decrease the activity of a serine/threonine kinase, comprising the steps of:

a. contacting a test compound with any polynucleotide of claim 1;

b. and detecting binding of the test compound to the polynucleotide, wherein a test compound which binds to the polynucleotide is identified as a potential therapeutic agent for decreasing the activity of serine/threonine kinase.

13. A method of reducing the activity of serine/threonine kinase, comprising the step of contacting a cell with a reagent which specifically binds to any polynucleotide of claim 1 or any serine/threonine kinase polypeptide of claim 4, whereby the activity of serine/threonine kinase is reduced.

14. A reagent that modulates the activity of a serine/threonine kinase polypeptide or a polynucleotide wherein said reagent is identified by the method of any of the claim 10 to 12.

15. A pharmaceutical composition, comprising the expression vector of claim 2 or the reagent of claim 14 and a pharmaceutically acceptable carrier.

16. Use of the expression vector of claim 2 or the reagent of claim 14 in the preparation of a medicament for modulating the activity of a serine/threonine kinase in a disease.

17. Use of claim 16 wherein the disease is cancer, diabetes, a CNS disorder or COPD.

Fig. 1

atgactctttcagatgacccagggcctatccgagatcagcttgttgttggacagctgattccagactgctatgtagaac
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Fig. 2

MTLSDDPGPIRDQLVVGQLIPDCYVELEKIILSERKNVPIEFPVIDRKRLLQLVRENQLQLDENELPHAVHFLNESDEN
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NEFDELEIQGKLPDPVKEYGCAPWPMVEKLIKQCLKENPQERPTSAQVFDILNSAELVCLTRRILLPKNVIVECMVATH
HNSRNASIWLGCGHTDRGQLSFLDLNTEGYTSEVNPNAL

Fig. 3

```
   1 mptqrwapgt qcmtkcensr pkpgelafrk gdmvtileac edkswyrakh hssgqeglla
  61 aaalrqreal stdpklslmp wfhgkisgqe aiqqlqpped glflvresar hpgdyvlcvs
 121 fgrdvihyrv lhrdghltid eavcfcnlmd mvehytrdkg aictklvkpk rkqgaksaee
 181 elakagwlld lqhltlgaqi gegefgavlq geylgqkvav knikcdvtaq afldetavmt
 241 klqhrnlvrl lgvilhhgly ivmehvskgn lvnflrtrgr alvstsqllq falhvaegme
 301 yleskklvhr dlaarnilvs edlvakvsdf glakaelrkg ldssrlpvkw tapealkngr
 361 fssksdvwsf gvllwevfsy grapypkmsl kevseavekg yrmeppdscp gpvhtlmgsc
 421 weaepsrrpp frkiveklgr elrsvgvaap aggqeaegsa ptrsqdp
```

Fig. 4

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Fig. 5

MTLSDDPGPVSLPELENSFFPEIRDQLVVGQLIPDCYVELEKIILSERKNVPIEFPVIDRKRLLQLVRENQLQLDENEL
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Fig. 6

MEEEEGAVAKEWGTTPAGPVWTAVFDYEAAGDEELTLRRGDRVQVLSQDCAVSGDEGWWTGQLPSGRVGVFPSNYVAPG
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PPEFPGRPTTLTFAPRPRPAASRPRLDPWKLVSFGRTLTISPPSRPDTPESPGPPSVQPTLLDMDMEGQNQDSTVPLCG
AHGSH

Fig. 7

MLGAIFERPIPPDTRPWYLHSAMIIYRDLKPHNVLLFTLYPNAAIIAKIADYGIAQYCCRMGIKTSEGTPGFRAPEVAR
GNVIYNQQADVYSFGLLLHDIWTTGSRIMEGLRFPNEFDELAIQGKLPDPVKEYGCAPWPMVEKLITKCLKENPQERPT
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KMRKTSVE

Fig. 8

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CCTTGGTGCATCTTCCTGTTGAAAAGGAAAGCTGGATTGTGTCTGGGACACAGTCTGGTACTCTCCTGGTCATCAATAC
CGAAGATGGGAAAAAGAGACATACCCTAGAAAAGATGACTGATTCTGTCACTTGTTTGTATTGCAATTCCTTTTCCAAG
CAAAGCAAACAAAAAAAATTTTCTTTTGGTTGGAACCGCTGATGGCAAGTTAGCAATTTTTGAAGATAAGACTGTTAAGC
TTAAAGGAGCTGCTCCTTTGAAGATACTAAATATAGGAAATGTCAGTACTCCATTGATGTGTTTGAGTGAATCCACAAA
TTCAACGGAAAGAAATGTAATGTGGGGAGGATGTGGCACAAAGATTTTCTCCTTTTCTAATGATTTCACCATTCAGAAA
CTCATTGAGACAAGAACAAGCCAACTGTTTTCTTATGCAGCTTTCAGTGATTCCAACATCATAACAGTGGTGGTAGACA
CTGCTCTCTATATTGCTAAGCAAAATAGCCCTGTTGTGGAAGTGTGGGATAAGAAAACTGAAAAACTCTGTGGACTAAT
AGACTGCGTGCACTTTTTAAGGGAGGTAATGGTAAAAGAAAACAAGGAATCAAAACACAAAATGTCTTATTCTGGGAGA

Fig. 8 (continued)

GTGAAAACCCTCTGCCTTCAGAAGAACACTGCTCTTTGGATAGGAACTGGAGGAGGCCATATTTTACTCCTGGATCTTT
CAACTCGTCGACTTATACGTGTAATTTACAACTTTTGTAATTCGGTCAGAGTCATGATGACAGCACAGCTAGGCAACCT
TAAAAATGTCATGCTGGTATTGGGCTACAACCGGAAAAATACTGAAGGTACACAAAAGCAGAAAGAGATACAATCTTGC
TTGACCGTTTGGGACATCAATCTTCCACATGAAGTGCAAAATTTAGAAAAACACATTGAAGTGAGAAAAGAATTAGCTG
AAAAAATGAGACGAACATCTGTTGAG

FIG. 9

BLASTP - alignment of 495 against swiss|P41243|MATK_RAT
MEGAKARYOCYTE-ASSOCIATED TYROSINE-PROTEIN KINASE (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE CTK) (PROTEIN KINASE BATK).//:trembl|L34542|RNBATK_1 gene: "batk"; product: "non-receptor protein kinase"; Rattus norvegicus non-receptor protein kinase (batk) gene, complete cds.
This hit is scoring at : 3e-23 (expectation value)
Alignment length (overlap) : 259
Identities : 29 %
Scoring matrix : BLOSUM62 (used to infer consensus pattern)
Database searched : nrdb_1_;

< ATP binding site: K >

Q: 270 LDDLMKKAE**EGDGSFGSVYRAAYEGEEVAVK**IFNKHTSLRLLRQELVVLCHLHHPSLISL
L..L. A: G:G.FG:V.:..Y G::VAV**K** .. ..:.:.. .E..V:..L.H :L:.L
H: 191 LQHLTLGAQ**IGEGEFGAV**LQGEYLGQKVAV**K**NIKCDVTAQAFLDETAVMTKLQHRNLVRL

< NP_Binding region >

LAAGIRPRM-LVMELASKGSLDRLLQQDKASLTRTLQ-HRIALHVADGLRYLHSAM**IIYR**
L.. :. : :VME .SKG:L ..L:. .:L..T Q :.ALHVA:G:.YL.S..:::R
LGVILHHGLYIVMEHVSKGNLVNFLRTRGRALVSTSQLLQFALHVAEGMEYLESKKLVHR

Fig. 9 (continued)

< serine/threonine specific pattern; active site: D >

```
          DLKPHNVLLFTLYPNAAIIAKIADYGIAQYCCRMGIKTSEGTPGFRAPEVARGNVIYNQQ
          DL...N:L:      :. ::AK::D:G:A:  .R.G:.:S. .  :.APE..: N  :::.:
          DLAARNILV-----SEDLVAKVSDFGLAKAELRKGLDSSRLPVKWTAPEALK-NGRFSSK

          ADVYSFGLLLYDILTTGGRIVEGLKFPNEFDELEIQGKLPDPVKEYGCAPWPMVEKLIKQ
          :DV:SFG:LL:::.: G . .. :.... :.:E   :::.P    ...P P V..L: .
          SDVWSFGVLLWEVFSYGRAPYPKMSLKEVSEAVEKGYRMEPP----DSCPGP-VHTLMGS

          CLKENPQERPTSAQVFDIL     526
          C :..P..RP. .::.: L
          CWEAEPSRRPPFRKIVEKL     438
```

FIG. 10

BLASTP - alignment of 495 against trembl|Z48615|HSMSTMR_1
gene: "MST"; product: "serine/threonine kinase with SH3 domain, leucine zip per domain and proline rich domain"; H.sapiens MST mRNA for serine/threonine kinase //:gp|Z48615|758593

This hit is scoring at : 1e-20 (expectation value)
Alignment length (overlap) : 287
Identities : 32 %
Scoring matrix : BLOSUM62 (used to infer consensus pattern)
Database searched : nrdb_1_;

```
Q:     266 QKILLDDLMKKAEEGDGSFGSVYRAAYEGEEVAVKIF------NKHTSLRLLRQELVVLC
           Q:I ..:L. :.  G G.FG.VYRA.:.GEEVAVK.        :. .:.. : QE. :.
H:      91 QEIPFHELQLEEIIGVGGFGKVYRALWRGEEVAVKAARLDPEKDPAVTAEQVCQEARLFG

           HLHHPSLISLLAAGIRP--RMLVMELASKGSLDRLLQQDKASLTRTLQHRI---ALHVAD
            L.HP::I:L .A :.P   .LVME.A. G:L.R:L      : .R. .H :   A:.VA
           ALQHPNIIALRGACLNPPHLCLVMEYARGGALSRVL-----AGRRVPPHVLVNWAVQVAR

           GLRYLHS---AMIIYRDLKPHNVLLFTLYPN---AAIIAKIADYGIAQYCCRMGIKTSEG
           G:.YLH:    . II:RDLK. N:L:.....N   A .:.KI.D:G:A:   :.   .:::.G
           GMNYLHNDAPVPIIHRDLKSINILILEAIENHNLADTVLKITDFGLAREWHKTTKMSAAG

           TPGFRAPEVARGNVIYNQQADVYSFGLLLYDILTTGGRIVEGLKFPNEFDELEI-----Q
           T .:.APEV.R : :::::.:DV:SFG:LL:::LT       G   .E.D.L.:      .
           TYAWMAPEVIRLS-LFSKSSDVWSFGVLLWELLT-------GEVPYREIDALAVAYGVAM

           GKLPDPVKEYGCAPWPMVEKLIKQCLKENPQERPTSAQVFDILNSAE      530
           .KL. P:.  ...P P.. :L:::C ..:P. RP. ..:.. L. .E
           NKLTLPIP--STCPEPFA-RLLEECWDPDPHGRPDFGSILKRLEVIE      361
```

FIG. 11

BLASTP - alignment of 495 against swissnew|P80192|M3K9_HUMAN
MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 9 (EC 2.7.1.-)
(MIXED LINEAGE KINASE 1) (FRAGMENT).//:swiss|P80192|M3K9_HUMAN
MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 9 (EC 2.7.1.-)
(MIXED LINEAGE KINASE 1) (FRAGMENT).

This hit is scoring at : 3e-22 (expectation value)
Alignment length (overlap) : 267
Identities : 32 %
Scoring matrix : BLOSUM62 (used to infer consensus pattern)
Database searched : nrdb_1_;

```
Q:     280 GDGSFGSVYRAAYEGEEVAVKIFNK------HTSLRLLRQELVVLCHLHHPSLISLLAAG
           G G.FG.VYRA : G:EVAVK. ..       ..:::. :RQE. :.. L.HP::I:L ..
H:      10 GIGGFGKVYRAFWIGDEVAVKAARHDPDEDISQTIENVRQEAKLFAMLKHPNIIALRGVC

IR-PRM-LVMELASKGSLDRLLQQDKASLTRTLQHRIALHVADGLRYLHS---AMIIYRD
:: P.: LVME.A. G.L:R:L. .:  :. .:   . A:.:A G:.YLH.   . II:RD
LKEPNLCLVMEFARGGPLNRVLSGKR--IPPDILVNWAVQIARGMNYLHDEAIVPIIHRD

LKPHNVLLFTLYPNAAI---IAKIADYGIAQYCCRMGIKTSEGTPGFRAPEVARGNVIYN
LK..N:L:.. ..N. :   I.KI.D:G:A:   R.  .:::.GT .:.APEV.R.: :::
LKSSNILILQKVENGDLSNKILKITDFGLAREWHRTTKMSAAGTYAWMAPEVIRAS-MFS

QQADVYSFGLLLYDILT--TGGRIVEGLKFPNEFDELEIQGKLPDPVKEYGCAPWPMVEK
: :DV:S:G:LL:::LT  .  R ::GL:..  .     ...KL. P:.  ...P P.. K
KGSDVWSYGVLLWELLTGEVPFRGIDGLRVAYGV----AMNKLALPIP--STCPEPFA-K

LIKQCLKENPQERPTSAQVFDILNSAE      530
L::.C ..:P..RP: ..:.D L.:.E
LMEDCWNPDPHSRPSFTNILDQLTTIE      266
```

FIG. 12

BLASTP - alignment of 495 against tremblnew|AK014886|AK014886_1
unnamed ORF; Mus musculus adult male testis cDNA, RIKEN full-length enriched library,
clone:4921513O20, full insert sequence.

This hit is scoring at : 5e-106 (expectation value)
Alignment length (overlap) : 209
Identities : 87 %
Scoring matrix : BLOSUM62 (used to infer consensus pattern)
Database searched : nrdb_1_;

```
Q:     378 YLHSAMIIYRDLKPHNVLLFTLYPNAAIIAKIADYGIAQYCCRMGIKTSEGTPGFRAPEV
           YLHSAMIIYRDLKPHNVLLFTLYPNAAIIAKIADYGIAQYCCRMGIKTSEGTPGFRAPEV
H:      18 YLHSAMIIYRDLKPHNVLLFTLYPNAAIIAKIADYGIAQYCCRMGIKTSEGTPGFRAPEV

           ARGNVIYNQQADVYSFGLLLYDILTTGGRIVEGLKFPNEFDELEIQGKLPDPVKEYGCAP
           ARGNVIYNQQADVYSFGLLL:DI TTG.RI:EGL:FPNEFDEL.IQGKLPDPVKEYGCAP
           ARGNVIYNQQADVYSFGLLLHDIWTTGSRIMEGLRFPNEFDELAIQGKLPDPVKEYGCAP

           WPMVEKLIKQCLKENPQERPTSAQVFDILNSAELVCLTRRILLPKNVIVECMVATHHNSR
           WPMVEKLI.:CLKENPQERPTSAQVFDILNSAEL:CL.R.IL:PKN:IVECMVAT: NS:
           WPMVEKLITKCLKENPQERPTSAQVFDILNSAELICLMRHILIPKNIIVECMVATNLNSK

           NASIWLGCGHTDRGQLSFLDLNTEGYTSE      586
           :A::WLGCG:T::GQLS..DLNTE Y: E
           SATLWLGCGNTEKGQLSLFDLNTERYSYE      226
```

Fig. 13

3D structure: BLASTP - alignment of 495 against pdb|1AGW|1AGW-B
fgf receptor 1fragment: tyrosine kinase domain; (fgfr1k)Mutant//:pdb|1FGI|1FGI-B fgf receptor 1fragment: tyrosine kinase domain; (fgfr1k)Mutant//:pdb|1FGK|1FGK-B fgf receptor 1fragment: tyrosine kinase domain, human fgfr1 residues that possess ptk activity; (fgfr1k, fibroblast growth factor receptor 1)Mutant//:pdb|2FGI|2FGI-B fibroblast growth factor (fgf) receptor 1fragment: tyrosine kinase domain; (fgfr1k)Mutant

This hit is scoring at : 2e-15 (expectation value)
Alignment length (overlap) : 267
Identities : 32 %
Scoring matrix : BLOSUM62 (used to infer consensus pattern)
Database searched : nrdb_1_;

```
Q:     280 GDGSFGSVYRAAYEG-----EEVAVKIFNKHTS---LRLLRQELVVLCHL-HHPSLISLL
           G:G:FG.V. A.  G      .:VAVK:.....:   L. L .E: ::  : .H.::I:LL
H:      25 GEGAFGQVVLAEAIGLPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLL

           AAGIR--PRMLVMELASKGSLDRLLQQDKASLTRTLQHRIALHVADGLRYLHSAMIIYRD
           .A .:  P .:::E.ASKG:L ..LQ. :.  ::.L . .A..VA G:.YL S...I:RD
           GACTQDGPLYVIVEYASKGNLREYLQARRQLSSKDLVS-CAYQVARGMEYLASKKCIHRD

           LKPHNVLLFTLYPNAAIIAKIADYGIAQYCCRMGIKTSEGTPGFRAPEVARGNVIYNQQA
           L...NVL:      ..  :.KIAD:G:A.Y     .K... .  :.APE A  : IY..Q:
           LAARNVLV-----TEDNVMKIADFGLADY-----YKKGRLPVKWMAPE-ALFDRIYTHQS

           DVYSFGLLLYDILTTGGRIVEGLKFPNEFDELEIQGKLPDPVKEYGCAPWPMVEKLIKQC
           DV:SFG:LL::I.T.GG. ..G:.... F. L: :G.  D  K. .C.    : .:::.C
           DVWSFGVLLWEIFTLGGSPYPGVPVEELFKLLK-EGHRMD--KPSNCT--NELYMMMRDC

           LKENPQERPTSAQVFDILNSAELVCLT     535
            .. P.:RPT .Q:.: L:  .:V.LT
           WHAVPSQRPTFKQLVEDLD--RIVALT     272
```

Fig. 14

HMMPFAM - alignment of 495 against pfam|hmm|pkinase
Protein kinase domain

This hit is scoring at : 136.1 E= 6.1e-37
Scoring matrix : BLOSUM62 (used to infer consensus pattern)

```
Q:     280 GDGSFGSVYRAAYE-GEEVAVKIFNKHTSLrllRQELVVLCHLHHPSLISLLAAGI---R
           G:GSFG.VY:A.:: G: VAVKI..K.:      :E: :L .L.HP:::.LL..
H:       8 GeGsfGkVykakhktgkivAvKilkkesls...lrEiqilkrlsHpNIvrllgvfedtdd

             PRMLVMELASKGSLDRLLQQDKaSLTRTLQHRIALHVADGLRYLHSAMIIYRDLKPHNVL
               .LVME... G.L  .L:::  .L:.. ..:IAL.:. GL.YLHS  I::RDLKP.N:L
             hlylvmEymegGdLfdylrrng.plsekeakkialQilrGleYLHsngivHRDLKpeNIL

             LFTLypnaaIIAKIADYGIAQYCcrMGIKTSEGTPGFR-APEV-ARGnVIYNQQADVYSF
             L .       ..KIAD:G:A:..    :.T  GTP :. APEV ..G   Y:.:.DV:S.
             lden.....gtvKiaDFGLArll..ekllttfvGTpwYmmAPEvileg.rgysskvDvWSl

             GLLLYDILTTG-----------GR------IVeGLKFPNE----------FDELEIQG
             G::LY::LT G             G       I.  LK.P .           .:EL
             GviLyElltggplfpgadlpaftggdevdqliif.vlklPfsdelpktridpleelfrik

             KLpDPVKEYGCAPWpmVEKLIKQCLKENPQERP---TSAQV     522
             K      . .C:.   ::.L:K:CL.::P.:RP   T:.::
             kr.rlplpsncSee..lkdLlkkcLnkDPskRpGsatakei     272
```

FIG. 15

BLASTP - alignment of 495_Protein against trembl|AK014886|AK014886_1
unnamed ORF; Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921513O20, full insert sequence. //:trembl|AK014938|AK014938_1 unnamed ORF; Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921521H10, full insert sequence.

This hit is scoring at : 0.0 (expectation value)
Alignment length (overlap) : 544
Identities : 85 %
Scoring matrix : BLOSUM62 (used to infer consensus pattern)
Database searched : nrdb_1_;

```
Q:     440 YLHSAMIIYRDLKPHNVLLFTLYPNAAIIAKIADYGIAQYCCRMGIKTSEGTPGFRAPEV
           YLHSAMIIYRDLKPHNVLLFTLYPNAAIIAKIADYGIAQYCCRMGIKTSEGTPGFRAPEV
H:      18 YLHSAMIIYRDLKPHNVLLFTLYPNAAIIAKIADYGIAQYCCRMGIKTSEGTPGFRAPEV

           ARGNVIYNQQADVYSFGLLLYDILTTGGRIVEGLKFPNEFDELEIQGKLPDPVKEYGCAP
           ARGNVIYNQQADVYSFGLLL:DI TTG.RI:EGL:FPNEFDEL.IQGKLPDPVKEYGCAP
           ARGNVIYNQQADVYSFGLLLHDIWTTGSRIMEGLRFPNEFDELAIQGKLPDPVKEYGCAP

           WPMVEKLIKQCLKENPQERPTSAQVFDILNSAELVCLTRRILLPKNVIVECMVATHHNSR
           WPMVEKLI.:CLKENPQERPTSAQVFDILNSAEL:CL.R.IL:PKN:IVECMVAT: NS:
           WPMVEKLITKCLKENPQERPTSAQVFDILNSAELICLMRHILIPKNIIVECMVATNLNSK

           NASIWLGCGHTDRGQLSFLDLNTEGYTSEEVADSRILCLALVHLPVEKESWIVSGTQSGT
           :A::WLGCG:T::GQLS..DLNTE Y: EEVADSRILCLALVHL..EKESW:V.GTQSG.
           SATLWLGCGNTEKGQLSLFDLNTERYSYEEVADSRILCLALVHLAAEKESWVVCGTQSGA

           LLVINTEDGKKRHTLEKMTDSVTCLYCNSFSKQSKQKNFLLVGTADGKLAIFEDKTVKLK
           LLVIN.E: .KRHTLEKMTDSVTCL:CNS.:KQSKQ.NFLLVGTADG.L.IFEDK.VK.K
           LLVINVEEETKRHTLEKMTDSVTCLHCNSLAKQSKQSNFLLVGTADGNLMIFEDKAVKCK
```

FIG. 15 (cont'd)

```
GAAPLKILNIGNVSTPLMCLSESTNSTERNVMWGGCGTKIFSFSNDFTIQKLIETRTSQL
GAAPLK.L:IG:VSTPLMCLSES.NS:ER::.WGGCGTK:FSFSNDFTIQKLIET:T:QL
GAAPLKTLHIGDVSTPLMCLSESLNSSERHITWGGCGTKVFSFSNDFTIQKLIETKTNQL

FSYAAFSDSNIITVVVDTALYIAKQNSPVVEVWDKKTEKLCGLIDCVHFLREVMVKENKE
FSYAAFSDSNII.:.VDTALYIAK:NSPVVEVWDKKTEKLC LIDCVHFL:EVMVK NKE
FSYAAFSDSNIIALAVDTALYIAKKNSPVVEVWDKKTEKLCELIDCVHFLKEVMVKLNKE

SKHKMSYSGRVKTLCLQKNTALWIGTGGGHILLLDLSTRRLIRVIYNFCNSVRVMMTAQL
SKH::SYSGRVK.LCLQKNTALWIGTGGGHILLLDLSTRR:IR.I:NFC:SVR.M.TAQL
SKHQLSYSGRVKALCLQKNTALWIGTGGGHILLLDLSTRRVIRTIHNFCDSVRAMATAQL

GSLKNVMLVLGYNRKNTEGTQKQKEIQSCLTVWDINLPHEVQNLEKHIEVRKELAEKMRR
GSLKNVMLVLGY.RK:TEG.Q:QKEIQSCL::WD:NLPHEVQNLEKHIEVR.ELA:KMR:
GSLKNVMLVLGYKRKSTEGIQEQKEIQSCLSIWDLNLPHEVQNLEKHIEVRTELADKMRK

TSVE      983
TSVE
TSVE      561
```

Fig. 16

Exon-intron structure prediction by Genewise: use mouse RIKEN sequence (trembl|AK014886|AK014886_1) as template on human clone refseq_hs_dna|NT_024370, assembled with a genscan output for the N-terminal region.
The following is the exon-intron boundary info of the putative full-length on chromosome 12q12.
Score 2082.81 bits over entire alignment
Scores as bits over a synchronous coding model

```
495p                    1 MTLSDDPGPVSLPELENSFFPE                                IRDQ
                          MTLSDDPGPVSLPELENSFFPE                                IRDQ
                          MTLSDDPGPVSLPELENSFFPE                                IRDQ
chr12:43154060- 9260 aactggcgcgaccgcgatttcgGTGCTTC  Intron 1   TAGacgc
                     tctcaacgctgtcataacttca<0-----[9326 :10855]-0>tgaa
                     gttatcagtgcgaatattcctg                                     catg

495p                   27 LVVGQLIPDCYVELEKIILSERKNVPIEFPVIDRKRLLQLVRENQLQLD
                          LVVGQLIPDCYVELEKIILSERKNVPIEFPVIDRKRLLQLVRENQLQLD
                          LVVGQLIPDCYVELEKIILSERKNVPIEFPVIDRKRLLQLVRENQLQLD
chr12:43154060-10868 cgggccacgttggcgaaattgcaagcagtcgagcacttccgagaccctg
                     tttgattcagatataatttcagaatctatcttagagttattgaaatata
                     tttaggtacctaataactaggtatgatatcatcgaaaaaagaatgggat

495p                   76 ENELPHAVHFLNES                                       VLLHFQDPA
                          ENELPHAVHFLNES                                       VLLHFQDPA
                          ENELPHAVHFLNES           G:G[gga]                    VLLHFQDPA
chr12:43154060-11015 gagcccggctcagtGGTTTGTG  Intron 2   CAGGAgccctcgcg
                     aaatcactattaac <1-----[11058:12095]-1>  tttataacc
                     atgttcatctataa                                             cttttacaa
```

FIG. 16 (cont'd)

```
495p                    100 LQLSDLYFVEPKWLCKIMAQ                                ILTVKV
                            LQLSDLYFVEPKWLCKIMAQ                                ILTVKV
                            LQLSDLYFVEPKWLCKIMAQ                                ILTVKV
chr12:43154060-12125        cctagtttggcatctaaagcGTTGGTG  Intron 3    CAGatagag
                            tatgatattacagtgattca<0-----[12185:16871]-0>ttctat
                            ggatcgctgacggttacgag                                tgagag

495p                    126 EGCPKHPKGIISRRDVEKFLSKKRKFPKNYMSQYFKLLEKFQIALPIGE
                            EGCPKHPKGIISRRDVEKFLSKKRKFPKNYMSQYFKLLEKFQIALPIGE
                            EGCPKHPKGIISRRDVEKFLSKKRKFPKNYMSQYFKLLEKFQIALPIGE
chr12:43154060-16890        ggtcaccagaatcagggatctaaaatcaatatcttaccgatcagtcagg
                            aggcaacagttcggataattcaagatcaaatcaatattaatatctctga
                            attaactgcttgtatgaattaaagatagccgagttgcaaacgttgaaaa

495p                    175 EYLLVPS                                     LSDHRPVIELPHCENS
                            EYLLVPS                                     LSDHRPVIELPHCENS
                            EYLLVPS                S:S[agt]             LSDHRPVIELPHCENS
chr12:43154060-17037        gttcgcaAGGTAAAGA  Intron 4    TAGTttgcacgagccctgat
                            aatttcg  <2-----[17060:17917]-2> tcaagcttatcagaac
                            atggtac                                     gtccgtgagtcttgct

495p                    199 EIIIRLYEMPYFPMGFWSRLINRLLEISPYMLSGR
                            EIIIRLYEMPYFPMGFWSRLINRLLEISPYMLSGR
                            EIIIRLYEMPYFPMGFWSRLINRLLEISPYMLSGR
chr12:43154060-17967        gaaacctgacttcagtttataactcgatctactga
                            atttgtaatcatctgtgcgttagttatccattcgg
                            atccaatagtttagatgaaactaatgtatcgtaga
```

Fig. 16 (continued)

```
495p                234                                  CILLGQVVDHIDSLMEEWFPGLL
                                                         CILLGQVVDHIDSLMEEWFPGLL
                                                         CILLGQVVDHIDSLMEEWFPGLL
                                   G:G[ggc]
chr12:43154060-18072 GGTAAGTA  Intron 5    TAGGCtactgcgggcagtcaggttcgtc
                      <1-----[18073:19202]-1>  gtttgattaatacttaagtcgtt
                                               tttgcatgcctttcgaagttggg

495p                258 EIDICGEGETLLKKWALYSFNDGEEHQKILLDDLMKKAEE
                        EIDICGEGETLLKKWALYSFNDGEEHQKILLDDLMKKAEE
                        EIDICGEGETLLKKWALYSFNDGEEHQKILLDDLMKKAEE
chr12:43154060-19274    gagatggggactaatgttatagggccaatcggtaaaggg
                        atatggagacttaagctagtaagaaaaatttaattaacaa
                        gtttttaaatgggagaatttttaataacattcgggaaga

495p                298                                  CFVCIHLYPSSDYISRHYMRTIN
                                                         CFVCIHLYPSSDYISRHYMRTIN
                                   D:D[gac]              CFVCIHLYPSSDYISRHYMRTIN
chr12:43154060-19394 GGTATGTT  Intron 6    TAGACttgtacttctagtatactaaaaa
                      <1-----[19395:23933]-1>  gttgtataccgaatcgaatgcta
                                               ttgttcataatcctagctgacat

495p                322 IVQTGFAKCRWRVTVHGADH                          DGS
                        IVQTGFAKCRWRVTVHGADH                          DGS
                        IVQTGFAKCRWRVTVHGADH          G:G[ggt]        DGS
chr12:43154060-24005    agcagtgatctagagcgggcGGTCAGTT  Intron 7   AAGGTgga
                        ttacgtcaggggtctagcaa <1-----[24066:25243]-1>  agg
                        taaaattatggaaaccgttt                          tct
```

Fig. 16 (continued)

```
495p                    346 FGSVYRAAYEGEEVAVKIFNKHTSLRLLRQ
                            FGSVYRAAYEGEEVAVKIFNKHTSLRLLRQ
                            FGSVYRAAYEGEEVAVKIFNKHTSLRLLRQ
chr12:43154060-25255        tgtgtcggtgggggggaataacatcactac
                            tgctagccaagaatctattaaacctgttga
                            taatcaactaaaagtggtttataacggaaa

495p                    376                                 ELVVLCHLHHPSLISLLAAGIRPRML
                                                            ELVVLCHLHHPSLISLLAAGIRPRML
                                                            ELVVLCHLHHPSLISLLAAGIRPRML
chr12:43154060-25345        GTAAGAA  Intron 8    CAGgcggctcccccatattcgggacccat
                            <0-----[25345:32005]-0>attttgataacgttcttccgtgcgtt
                                                            gtggtccccccctgatggatgttcggg


495p                    402 VMELASKGSLDRLLQQDKASLTRTLQHRIALHVADGL
                            VMELASKGSLDRLLQQDKASLTRTLQHRIALHVADGL
chr12:43154060-32084        gagtgtagttgcccccgagacaaacccaagccggggt
                            ttatccagctagttaaaacgtcgctaagtctatcagt
                            gggaccgtcgtcgtggcaccctacagcgtaccatttg

495p                    439                                 YLHSAMIIYRDLKPHNVLLFTLY
                                                            YLHSAMIIYRDLKPHNVLLFTLY
                                      R:R[aga]              YLHSAMIIYRDLKPHNVLLFTLY
chr12:43154060-32195        AGGTAAGTA  Intron 9    CAGAtcctgaaatcgcaccagcctact
                              <2-----[32197:37333]-2> ataccttagatacaatttctta
                                                            cccacgtacacgacctggtcagt
```

Fig. 16 (continued)

```
495p                463 PNAAIIAKIADYGIAQYCCRMGIKTSEGTP
                        PNAAIIAKIADYGIAQYCCRMGIKTSEGTP
                        PNAAIIAKIADYGIAQYCCRMGIKTSEGTP
chr12:43154060-37404    caggaagaaggtgagctttaagaaatggac
                        caccttcatcaagtcaagggtgtaccagcc
                        cttcctagttcccttgcctaggaaaagcaa

495p                493                                 FRAPEVARGNVIYNQQADVYSFG
                                                        FRAPEVARGNVIYNQQADVYSFG
                                  G:G[ggg]              FRAPEVARGNVIYNQQADVYSFG
chr12:43154060-37494 GGTAGGTG   Intron 10   CAGGGtcgcgggagagataccgggtttg
                      <1-----[37495:43792]-1>  tgccatcggattaaaacatactg
                                               ttatatcaatcttcagttttatt

495p                517 LLLYDILTTGGRIVEGLKFPNEFDELEIQGKLP
                        LLLYDILTTGGRIVEGLKFPNEFDELEIQGKLP
                        LLLYDILTTGGRIVEGLKFPNEFDELEIQGKLP
chr12:43154060-43864    tcctgataaggaagggtatcagtggtgacgatc
                        tttaattccgggttagtatcaataatatagatc
                        aactctgatataaagtggtatgttaaaaaaaat

495p                550                                 PVKEYGCAPWPMVEKLIKQCLKE
                                                        PVKEYGCAPWPMVEKLIKQCLKE
                                  D:D[gat]              PVKEYGCAPWPMVEKLIKQCLKE
chr12:43154060-43963 GGTAAGTT   Intron 11   TAGATcgagtgtgctcaggataacttag
                      <1-----[43964:45448]-1>  ctaaaggccgcttaattaagtaa
                                               ataatttcagtgtgaatagtgaa
```

Fig. 16 (continued)

```
495p                    574 NPQERPTSAQ                                  VFDILNSAELVCLTRR
                            NPQERPTSAQ                                  VFDILNSAELVCLTRR
                            NPQERPTSAQ                                  VFDILNSAELVCLTRR
chr12:43154060-45520        accgacatgcGTATTCT  Intron 12  CAGgtgatatggtgtcaac
                            acaagcccca<0-----[45550:48581]-0>ttattaccattgtcgg
                            ttaagtttcg                                  ctctgtataactggac

495p                    600 ILLPKNVIVECMVATHHNSRNASIWLGCGHTDRGQLSFLDLNTEGYTSE
                            ILLPKNVIVECMVATHHNSRNASIWLGCGHTDRGQLSFLDLNTEGYTSE
                            ILLPKNVIVECMVATHHNSRNASIWLGCGHTDRGQLSFLDLNTEGYTSE
chr12:43154060-48630        attcaagaggtaggaccaaaagaatcgtgcagagccttcgtaaggtatg
                            tttcaatttagttccaaaggacgtgtgggacaggatcttatacagacca
                            taatacattacgttatcccgtactggctgcccaagcattcattaacttg

495p                    649                                 EVADSRILCLALVHLPVEKESWIVSG
                                                            EVADSRILCLALVHLPVEKESWIVSG
                                                            EVADSRILCLALVHLPVEKESWIVSG
chr12:43154060-48777        GTAAATC  Intron 13  CAGggggaaatttgtgcccggagatagtg
                            <0-----[48777:51341]-0>atcaggttgtcttatctaaaggttcg
                                                            attttaagcacggttttagacgtgtg

495p                    675 TQSGTLLVINTEDGKKRHTLEKMTDSVTCLYCNSFSKQ
                            TQSGTLLVINTEDGKKRHTLEKMTDSVTCLYCNSFSKQ
                            TQSGTLLVINTEDGKKRHTLEKMTDSVTCLYCNSFSKQ
chr12:43154060-51420        actgaccgaaagggaaacacgaaagtgattttatttac
                            cacgcttttacaagaagactaatcactcgtagactcaa
                            agtttcgcctcatgagatcaaggtttcttgtctctcga
```

Fig. 16 (continued)

```
495p                 713                                  KQKNFLLVGTADGKLAIFEDKTV
                                                          KQKNFLLVGTADGKLAIFEDKTV
                                                          KQKNFLLVGTADGKLAIFEDKTV
                                    S:S[agc]
chr12:43154060-51534 AGGTATGGT  Intron 14  TAGCacaatctggagggatgatggaag
                       <2-----[51536:53157]-2> aaaattttgccagatcttaaact
                                                aaatttgtacttcgaattatgtt

495p                 737 K                      LKGAAPLKILNIGNVSTPLMCLSES
                         K                      LKGAAPLKILNIGNVSTPLMCLSES
                         K                      LKGAAPLKILNIGNVSTPLMCLSES
chr12:43154060-53228 aGTAAATG  Intron 15  AAGcagggctaacaagagaactattagt
                         a<0-----[53231:56302]-0>tagccctattatgatgccttgtgac
                         g                      taatttggaataatcttaggtgtac

495p                 763 TNSTERNVMWGGCGTKIFSFSNDFTIQKLIETRTSQ
                         TNSTERNVMWGGCGTKIFSFSNDFTIQKLIETRTSQ
                         TNSTERNVMWGGCGTKIFSFSNDFTIQKLIETRTSQ
chr12:43154060-56378 aatagaagatggtgaaattttagtaacacagaaaac
                         caccagattgggggcattctcaatctaattacgcga
                         atagaataggaatcagtccttttcctgactgaaaca

495p                 799                              FSYAAFSDSNIITVVVDTALYIA
                                                      FSYAAFSDSNIITVVVDTALYIA
                                    L:L[ctg]          FSYAAFSDSNIITVVVDTALYIA
chr12:43154060-56486 CTGTAAGTT  Intron 16  TAGGtttggtagtaaaaggggagctag
                       <2-----[56488:60444]-2> tcacctgacattctttacctatc
                                                tttatcttcccaaggacttcttt
```

Fig. 16 (continued)

```
495p                        823 KQNSPVVEVWDKKTEKLCGLIDCVHFL
                                KQNSPVVEVWDKKTEKLCGLIDCVHFL
                                KQNSPVVEVWDKKTEKLCGLIDCVHFL                R:R[agg]
chr12:43154060-60515            acaacggggtgaaagactgcagtgcttAGGTAAATT  Intron 17
                                aaagcttatgaaacaatggttagtatt  <2-----[60598:61884]
                                gatcttgaggtgataactaaaccgcta

495p                        850     EVMVKENKESKHKMSYSGRVKTLCLQKNTALWIGTGGGHILLLDL
                                    EVMVKENKESKHKMSYSGRVKTLCLQKNTALWIGTGGGHILLLDL
                                    EVMVKENKESKHKMSYSGRVKTLCLQKNTALWIGTGGGHILLLDL
chr12:43154060-61882            TAGGgagagaagtacaatttgagaactccaaagctagagggcatccgc
                                -2> atttaaaaacaaatcacggtactgtaaacctgtgcgggattttat
                                    gagaaacgaaacagtttgagaccctggctttgaataacttacgtt

495p                        896 STRRLIRVIYNFCNSVRVMMTAQLG
                                STRRLIRVIYNFCNSVRVMMTAQLG
                                STRRLIRVIYNFCNSVRVMMTAQLG                  S:N[aac]
chr12:43154060-62021            tacccacgatattatgagaaagccgAAGTTTCTT  Intron 18
                                ccggttgttaatgactgtttccatg  <2-----[62098:64052]
                                attatatatcctttgcacggaagac

495p                        921     LKNVMLVLGYNRKNTEGTQKQK
                                    LKNVMLVLGYNRKNTEGTQKQK
                                    LKNVMLVLGYNRKNTEGTQKQK                 E:E[gag]
chr12:43154060-64050            AAGCcaagacgtgtacaaaggacacaGGTAACAT  Intron 19
                                -2> taatttttgaagaacagcaaaa <1-----[64121:64686]
                                    tatcggagcccgattataagga
```

Fig. 16 (continued)

```
495p                    944       IQSCLTVWDINLPHEVQNLEKHIEVRKELAEKMRRTSVE
                                  IQSCLTVWDINLPHEVQNLEKHIEVRKELAEKMRRTSVE
                                  IQSCLTVWDINLPHEVQNLEKHIEVRKELAEKMRRTSVE
chr12:43154060-64684 TAGAGactttagtgaacccggcatgacaggaagtggaaacatgg
                     -1>  tacgtctgatatcaataataaatatgaatcaatggccta
                          aatcgctgccttatagataaactagaaaataagaaattg
```

Fig. 17

Lane Number	Sample	Relative Expression		Absolute Expression	
1	Adrenal gland	8.064286		112.9	
2	Bone marrow	21.057142		294.8	
3	Brain	4.4928575		62.9	
4	Colon	5.6142855		78.6	
5	Heart	15.1285715		211.8	
6	Kidney	26.47143		370.6	
7	Liver	1.1214286		15.7	
8	Lung	33.485714		468.8	
9	Mammary gland	6.8785715		96.3	
10 (Control)	Ovary	1.0		14.0	
11	Pancreas	2.6357143		36.9	
12	Prostate	10.735715		150.3	
13	Salivary gland	13.071428		183.0	
14	Skeletal Muscle	14.2		198.8	
15	Sm Intest	8.328571		116.6	
16	Spinal Cord	32.435715		454.1	
17	Spleen	62.82143		879.5	
18	Stomach	13.664286		191.3	
19	Testis	21.6		302.4	
20	Thymus	18.192858		254.7	
21	Thyroid	3.1499999		44.1	
22	Trachea	8.542857		119.6	
23	Uterus	3.207143		44.9	

Fig. 18

Lane Number	Sample	Relative Expression		Absolute Expression	
1	Lung	127.57952		585.59	
2	Trachea	17.67538		81.13	
3	HBEC 2	62.213505		285.56	
4	H441	0.0		0.0	
5	SMC	29.764704		136.62	
6 (Control)	SAE	1.0		4.59	
7	AII	24.75599		113.63	
8	Foetal lung	1483.196		6807.87	
9	Fibroblast	6.769063		31.07	
10	PMN 1	4259.7383		19552.2	
11	PMN 2	533.1089		2446.97	
12	PMN 3	68.43573		314.12	
13	Mono 1	92.84967		426.18	
14	Mono 2	39.620914		181.86	
15	Mono 3	17.90196		82.17	
16	Cult. Mono 1	42.76035		196.27	
17	Cult. Mono 2	51.742916		237.5	
18	Tcell 1	8.457516		38.82	
19	Tcell 2	14.24183		65.37	

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Pro Tyr Met Leu Ser Gly Arg Gly Cys Ile Leu Leu Gly Gln Val Val
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545                 550                 555                 560

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ggactaatag actgcgtgca ctttttaagg gaggtaatgg taaaagaaaa caaggaatca 2580

aaacacaaaa tgtcttattc tgggagagtg aaaaccctct gccttcagaa gaacactgct 2640

ctttggatag gaactggagg aggccatatt ttactcctgg atctttcaac tcgtcgactt 2700

atacgtgtaa tttacaactt ttgtaattcg gtcagagtca tgatgacagc acagctaggc 2760

aaccttaaaa atgtcatgct ggtattgggc tacaaccgga aaaatactga aggtacacaa 2820

aagcagaaag agatacaatc ttgcttgacc gtttgggaca tcaatcttcc acatgaagtg 2880

caaaatttag aaaaacacat tgaagtgaga 2910

<210> 5

<211> 983

<212> PRT

<213> Homo sapiens

<400> 5

Met Thr Leu Ser Asp Asp Pro Gly Pro Val Ser Leu Pro Glu Leu Glu
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Asn Ser Phe Phe Pro Glu Ile Arg Asp Gln Leu Val Val Gly Gln Leu
20 25 30

Ile Pro Asp Cys Tyr Val Glu Leu Glu Lys Ile Ile Leu Ser Glu Arg

35 40 45

Lys Asn Val Pro Ile Glu Phe Pro Val Ile Asp Arg Lys Arg Leu Leu
50 55 60

Gln Leu Val Arg Glu Asn Gln Leu Gln Leu Asp Glu Asn Glu Leu Pro
65 70 75 80

His Ala Val His Phe Leu Asn Glu Ser Gly Val Leu Leu His Phe Gln
85 90 95

Asp Pro Ala Leu Gln Leu Ser Asp Leu Tyr Phe Val Glu Pro Lys Trp
100 105 110

Leu Cys Lys Ile Met Ala Gln Ile Leu Thr Val Lys Val Glu Gly Cys
115 120 125

Pro Lys His Pro Lys Gly Ile Ile Ser Arg Arg Asp Val Glu Lys Phe
130 135 140

Leu Ser Lys Lys Arg Lys Phe Pro Lys Asn Tyr Met Ser Gln Tyr Phe
145 150 155 160

Lys Leu Leu Glu Lys Phe Gln Ile Ala Leu Pro Ile Gly Glu Glu Tyr
165 170 175

Leu Leu Val Pro Ser Ser Leu Ser Asp His Arg Pro Val Ile Glu Leu
180 185 190

Pro His Cys Glu Asn Ser Glu Ile Ile Ile Arg Leu Tyr Glu Met Pro
195 200 205

Tyr Phe Pro Met Gly Phe Trp Ser Arg Leu Ile Asn Arg Leu Leu Glu
210 215 220

Ile Ser Pro Tyr Met Leu Ser Gly Arg Gly Cys Ile Leu Leu Gly Gln
225 230 235 240

Val Val Asp His Ile Asp Ser Leu Met Glu Glu Trp Phe Pro Gly Leu
245 250 255

Leu Glu Ile Asp Ile Cys Gly Glu Gly Glu Thr Leu Leu Lys Lys Trp
260 265 270

Ala Leu Tyr Ser Phe Asn Asp Gly Glu Glu His Gln Lys Ile Leu Leu
275 280 285

Asp Asp Leu Met Lys Lys Ala Glu Glu Asp Cys Phe Val Cys Ile His
290 295 300

Leu Tyr Pro Ser Ser Asp Tyr Ile Ser Arg His Tyr Met Arg Thr Ile
305 310 315 320

Asn Ile Val Gln Thr Gly Phe Ala Lys Cys Arg Trp Arg Val Thr Val
325 330 335

His Gly Ala Asp His Gly Asp Gly Ser Phe Gly Ser Val Tyr Arg Ala
340 345 350

Ala Tyr Glu Gly Glu Glu Val Ala Val Lys Ile Phe Asn Lys His Thr
355 360 365

Ser Leu Arg Leu Leu Arg Gln Glu Leu Val Val Leu Cys His Leu His
370 375 380

His Pro Ser Leu Ile Ser Leu Leu Ala Ala Gly Ile Arg Pro Arg Met
385 390 395 400

Leu Val Met Glu Leu Ala Ser Lys Gly Ser Leu Asp Arg Leu Leu Gln
405 410 415

Gln Asp Lys Ala Ser Leu Thr Arg Thr Leu Gln His Arg Ile Ala Leu
420 425 430

His Val Ala Asp Gly Leu Arg Tyr Leu His Ser Ala Met Ile Ile Tyr
435 440 445

Arg Asp Leu Lys Pro His Asn Val Leu Leu Phe Thr Leu Tyr Pro Asn
450 455 460

Ala Ala Ile Ile Ala Lys Ile Ala Asp Tyr Gly Ile Ala Gln Tyr Cys
465 470 475 480

Cys Arg Met Gly Ile Lys Thr Ser Glu Gly Thr Pro Gly Phe Arg Ala
485 490 495

Pro Glu Val Ala Arg Gly Asn Val Ile Tyr Asn Gln Gln Ala Asp Val
500 505 510

Tyr Ser Phe Gly Leu Leu Leu Tyr Asp Ile Leu Thr Thr Gly Gly Arg
515 520 525

Ile Val Glu Gly Leu Lys Phe Pro Asn Glu Phe Asp Glu Leu Glu Ile
530 535 540

Gln Gly Lys Leu Pro Asp Pro Val Lys Glu Tyr Gly Cys Ala Pro Trp
545 550 555 560

Pro Met Val Glu Lys Leu Ile Lys Gln Cys Leu Lys Glu Asn Pro Gln
565 570 575

Glu Arg Pro Thr Ser Ala Gln Val Phe Asp Ile Leu Asn Ser Ala Glu
580 585 590

Leu Val Cys Leu Thr Arg Arg Ile Leu Leu Pro Lys Asn Val Ile Val
595 600 605

Glu Cys Met Val Ala Thr His His Asn Ser Arg Asn Ala Ser Ile Trp
610 615 620

Leu Gly Cys Gly His Thr Asp Arg Gly Gln Leu Ser Phe Leu Asp Leu
625 630 635 640

Asn Thr Glu Gly Tyr Thr Ser Glu Glu Val Ala Asp Ser Arg Ile Leu
645 650 655

Cys Leu Ala Leu Val His Leu Pro Val Glu Lys Glu Ser Trp Ile Val
660 665 670

Ser Gly Thr Gln Ser Gly Thr Leu Leu Val Ile Asn Thr Glu Asp Gly
675 680 685

Lys Lys Arg His Thr Leu Glu Lys Met Thr Asp Ser Val Thr Cys Leu
690 695 700

Tyr Cys Asn Ser Phe Ser Lys Gln Ser Lys Gln Lys Asn Phe Leu Leu
705 710 715 720

Val Gly Thr Ala Asp Gly Lys Leu Ala Ile Phe Glu Asp Lys Thr Val
725 730 735

Lys Leu Lys Gly Ala Ala Pro Leu Lys Ile Leu Asn Ile Gly Asn Val
740 745 750

Ser Thr Pro Leu Met Cys Leu Ser Glu Ser Thr Asn Ser Thr Glu Arg
755 760 765

Asn Val Met Trp Gly Gly Cys Gly Thr Lys Ile Phe Ser Phe Ser Asn
770 775 780

Asp Phe Thr Ile Gln Lys Leu Ile Glu Thr Arg Thr Ser Gln Leu Phe
785 790 795 800

Ser Tyr Ala Ala Phe Ser Asp Ser Asn Ile Ile Thr Val Val Val Asp
805 810 815

Thr Ala Leu Tyr Ile Ala Lys Gln Asn Ser Pro Val Val Glu Val Trp
820 825 830

Asp Lys Lys Thr Glu Lys Leu Cys Gly Leu Ile Asp Cys Val His Phe
835 840 845

Leu Arg Glu Val Met Val Lys Glu Asn Lys Glu Ser Lys His Lys Met
850 855 860

Ser Tyr Ser Gly Arg Val Lys Thr Leu Cys Leu Gln Lys Asn Thr Ala
865 870 875 880

Leu Trp Ile Gly Thr Gly Gly Gly His Ile Leu Leu Leu Asp Leu Ser
885 890 895

Thr Arg Arg Leu Ile Arg Val Ile Tyr Asn Phe Cys Asn Ser Val Arg
900 905 910

Val Met Met Thr Ala Gln Leu Gly Ser Leu Lys Asn Val Met Leu Val
915 920 925

Leu Gly Tyr Asn Arg Lys Asn Thr Glu Gly Thr Gln Lys Gln Lys Glu
930 935 940

Ile Gln Ser Cys Leu Thr Val Trp Asp Ile Asn Leu Pro His Glu Val
945 950 955 960

Gln Asn Leu Glu Lys His Ile Glu Val Arg Lys Glu Leu Ala Glu Lys
965 970 975

Met Arg Arg Thr Ser Val Glu

980

<210> 6

<211> 953

<212> PRT

<213> Homo sapiens

<400> 6

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Ala Gly Pro Val Trp Thr Ala Val Phe Asp Tyr Glu Ala Ala Gly Asp
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Glu Glu Leu Thr Leu Arg Arg Gly Asp Arg Val Gln Val Leu Ser Gln
35 40 45

Asp Cys Ala Val Ser Gly Asp Glu Gly Trp Trp Thr Gly Gln Leu Pro
50 55 60

Ser Gly Arg Val Gly Val Phe Pro Ser Asn Tyr Val Ala Pro Gly Ala
65 70 75 80

Pro Ala Ala Pro Ala Gly Leu Gln Leu Pro Gln Glu Ile Pro Phe His
85 90 95

Glu Leu Gln Leu Glu Glu Ile Ile Gly Val Gly Gly Phe Gly Lys Val
100 105 110

Tyr Arg Ala Leu Trp Arg Gly Glu Glu Val Ala Val Lys Ala Ala Arg
115 120 125

Leu Asp Pro Glu Lys Asp Pro Ala Val Thr Ala Glu Gln Val Cys Gln
130 135 140

Glu Ala Arg Leu Phe Gly Ala Leu Gln His Pro Asn Ile Ile Ala Leu
145 150 155 160

Arg Gly Ala Cys Leu Asn Pro Pro His Leu Cys Leu Val Met Glu Tyr
165 170 175

Ala Arg Gly Gly Ala Leu Ser Arg Val Leu Ala Gly Arg Arg Val Pro
180 185 190

Pro His Val Leu Val Asn Trp Ala Val Gln Val Ala Arg Gly Met Asn
195 200 205

Tyr Leu His Asn Asp Ala Pro Val Pro Ile Ile His Arg Asp Leu Lys
210 215 220

Ser Ile Asn Ile Leu Ile Leu Glu Ala Ile Glu Asn His Asn Leu Ala
225 230 235 240

Asp Thr Val Leu Lys Ile Thr Asp Phe Gly Leu Ala Arg Glu Trp His
245 250 255

Lys Thr Thr Lys Met Ser Ala Ala Gly Thr Tyr Ala Trp Met Ala Pro
260 265 270

Glu Val Ile Arg Leu Ser Leu Phe Ser Lys Ser Ser Asp Val Trp Ser
275 280 285

Phe Gly Val Leu Leu Trp Glu Leu Leu Thr Gly Glu Val Pro Tyr Arg
290 295 300

Glu Ile Asp Ala Leu Ala Val Ala Tyr Gly Val Ala Met Asn Lys Leu
305 310 315 320

Thr Leu Pro Ile Pro Ser Thr Cys Pro Glu Pro Phe Ala Arg Leu Leu
325 330 335

Glu Glu Cys Trp Asp Pro Asp Pro His Gly Arg Pro Asp Phe Gly Ser
340 345 350

Ile Leu Lys Arg Leu Glu Val Ile Glu Gln Ser Ala Leu Phe Gln Met
355 360 365

Pro Leu Glu Ser Phe His Ser Leu Gln Glu Asp Trp Lys Leu Glu Ile
370 375 380

Gln His Met Phe Asp Asp Leu Arg Thr Lys Glu Lys Glu Leu Arg Ser
385 390 395 400

Arg Glu Glu Glu Leu Leu Arg Ala Ala Gln Glu Gln Arg Phe Gln Glu
405 410 415

Glu Gln Leu Arg Arg Arg Glu Gln Glu Leu Ala Glu Arg Glu Met Asp
420 425 430

Ile Val Glu Arg Glu Leu His Leu Leu Met Cys Gln Leu Ser Gln Glu
435 440 445

Lys Pro Arg Val Arg Lys Arg Lys Gly Asn Phe Lys Arg Ala Val Leu
450 455 460

Lys Leu Arg Glu Gly Ser Ser His Ile Ser Leu Pro Ser Gly Phe Glu
465 470 475 480

His Lys Ile Thr Val Gln Ala Ser Pro Thr Leu Asp Lys Arg Lys Gly
485 490 495

Ser Asp Gly Ala Ser Pro Pro Ala Ser Pro Ser Ile Ile Pro Arg Leu
500 505 510

Arg Ala Ile Arg Leu Thr Pro Val Asp Cys Gly Gly Ser Ser Ser Gly
515 520 525

Ser Ser Ser Gly Gly Ser Gly Thr Trp Ser Arg Gly Gly Pro Pro Lys
530 535 540

Lys Glu Glu Leu Val Gly Gly Lys Lys Lys Gly Arg Thr Trp Gly Pro
545 550 555 560

Ser Ser Thr Leu Gln Lys Glu Arg Val Gly Gly Glu Glu Arg Leu Lys
565 570 575

Gly Leu Gly Glu Gly Ser Lys Gln Trp Ser Ser Ser Ala Pro Asn Leu
580 585 590

Gly Lys Ser Pro Lys His Thr Pro Ile Ala Pro Gly Phe Ala Ser Leu
595 600 605

Asn Glu Met Glu Glu Phe Ala Glu Ala Glu Asp Gly Gly Ser Ser Val
610 615 620

Pro Pro Ser Pro Tyr Ser Thr Pro Ser Tyr Leu Ser Val Pro Leu Pro
625 630 635 640

Ala Glu Pro Ser Pro Gly Ala Arg Ala Pro Trp Glu Pro Thr Pro Ser
645 650 655

Ala Pro Pro Ala Arg Trp Gly His Gly Ala Arg Arg Arg Cys Asp Leu
660 665 670

Ala Leu Leu Gly Cys Ala Thr Leu Leu Gly Ala Val Gly Leu Gly Ala
675 680 685

Asp Val Ala Glu Ala Arg Ala Ala Asp Gly Glu Glu Gln Arg Arg Trp
690 695 700

Leu Asp Gly Leu Phe Phe Pro Arg Ala Gly Arg Phe Pro Arg Gly Leu
705 710 715 720

Ser Pro Pro Ala Arg Pro His Gly Arg Arg Glu Asp Val Gly Pro Gly
725 730 735

Leu Gly Leu Ala Pro Ser Ala Thr Leu Val Ser Leu Ser Ser Val Ser
740 745 750

Asp Cys Asn Ser Thr Arg Ser Leu Leu Arg Ser Asp Ser Asp Glu Ala
755 760 765

Ala Pro Ala Ala Pro Ser Pro Pro Pro Ser Pro Pro Ala Pro Thr Pro
770 775 780

Thr Pro Ser Pro Ser Thr Asn Pro Leu Val Asp Leu Glu Leu Glu Ser
785 790 795 800

Phe Lys Lys Asp Pro Arg Gln Ser Leu Thr Pro Thr His Val Thr Ala
805 810 815

Ala Cys Ala Val Ser Arg Gly His Arg Arg Thr Pro Ser Asp Gly Ala
820 825 830

Leu Gly Gln Arg Gly Pro Pro Glu Pro Ala Gly His Gly Pro Gly Pro
835 840 845

Arg Asp Leu Leu Asp Phe Pro Arg Leu Pro Asp Pro Gln Ala Leu Phe
850 855 860

Pro Ala Arg Arg Arg Pro Pro Glu Phe Pro Gly Arg Pro Thr Thr Leu
865 870 875 880

Thr Phe Ala Pro Arg Pro Arg Pro Ala Ala Ser Arg Pro Arg Leu Asp

885 890 895

Pro Trp Lys Leu Val Ser Phe Gly Arg Thr Leu Thr Ile Ser Pro Pro
900 905 910

Ser Arg Pro Asp Thr Pro Glu Ser Pro Gly Pro Pro Ser Val Gln Pro
915 920 925

Thr Leu Leu Asp Met Asp Met Glu Gly Gln Asn Gln Asp Ser Thr Val
930 935 940

Pro Leu Cys Gly Ala His Gly Ser His
945 950

<210> 7

<211> 561

<212> PRT

<213> Homo sapiens

<400> 7

Met Leu Gly Ala Ile Phe Glu Arg Pro Ile Pro Pro Asp Thr Arg Pro
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Trp Tyr Leu His Ser Ala Met Ile Ile Tyr Arg Asp Leu Lys Pro His
20 25 30

Asn Val Leu Leu Phe Thr Leu Tyr Pro Asn Ala Ala Ile Ile Ala Lys
35 40 45

Ile Ala Asp Tyr Gly Ile Ala Gln Tyr Cys Cys Arg Met Gly Ile Lys
50 55 60

Thr Ser Glu Gly Thr Pro Gly Phe Arg Ala Pro Glu Val Ala Arg Gly
65 70 75 80

Asn Val Ile Tyr Asn Gln Gln Ala Asp Val Tyr Ser Phe Gly Leu Leu
85 90 95

Leu His Asp Ile Trp Thr Thr Gly Ser Arg Ile Met Glu Gly Leu Arg
100 105 110

Phe Pro Asn Glu Phe Asp Glu Leu Ala Ile Gln Gly Lys Leu Pro Asp
115 120 125

Pro Val Lys Glu Tyr Gly Cys Ala Pro Trp Pro Met Val Glu Lys Leu
130 135 140

Ile Thr Lys Cys Leu Lys Glu Asn Pro Gln Glu Arg Pro Thr Ser Ala
145 150 155 160

Gln Val Phe Asp Ile Leu Asn Ser Ala Glu Leu Ile Cys Leu Met Arg
165 170 175

His Ile Leu Ile Pro Lys Asn Ile Ile Val Glu Cys Met Val Ala Thr
180 185 190

Asn Leu Asn Ser Lys Ser Ala Thr Leu Trp Leu Gly Cys Gly Asn Thr
195 200 205

Glu Lys Gly Gln Leu Ser Leu Phe Asp Leu Asn Thr Glu Arg Tyr Ser
210 215 220

Tyr Glu Glu Val Ala Asp Ser Arg Ile Leu Cys Leu Ala Leu Val His
225 230 235 240

Leu Ala Ala Glu Lys Glu Ser Trp Val Val Cys Gly Thr Gln Ser Gly
245 250 255

Ala Leu Leu Val Ile Asn Val Glu Glu Glu Thr Lys Arg His Thr Leu
260 265 270

Glu Lys Met Thr Asp Ser Val Thr Cys Leu His Cys Asn Ser Leu Ala
275 280 285

Lys Gln Ser Lys Gln Ser Asn Phe Leu Leu Val Gly Thr Ala Asp Gly
290 295 300

Asn Leu Met Ile Phe Glu Asp Lys Ala Val Lys Cys Lys Gly Ala Ala
305 310 315 320

Pro Leu Lys Thr Leu His Ile Gly Asp Val Ser Thr Pro Leu Met Cys
325 330 335

Leu Ser Glu Ser Leu Asn Ser Ser Glu Arg His Ile Thr Trp Gly Gly
340 345 350

Cys Gly Thr Lys Val Phe Ser Phe Ser Asn Asp Phe Thr Ile Gln Lys
355 360 365

Leu Ile Glu Thr Lys Thr Asn Gln Leu Phe Ser Tyr Ala Ala Phe Ser
370 375 380

Asp Ser Asn Ile Ile Ala Leu Ala Val Asp Thr Ala Leu Tyr Ile Ala
385 390 395 400

Lys Lys Asn Ser Pro Val Val Glu Val Trp Asp Lys Lys Thr Glu Lys
405 410 415

Leu Cys Glu Leu Ile Asp Cys Val His Phe Leu Lys Glu Val Met Val
420 425 430

Lys Leu Asn Lys Glu Ser Lys His Gln Leu Ser Tyr Ser Gly Arg Val
435 440 445

Lys Ala Leu Cys Leu Gln Lys Asn Thr Ala Leu Trp Ile Gly Thr Gly
450 455 460

Gly Gly His Ile Leu Leu Leu Asp Leu Ser Thr Arg Arg Val Ile Arg
465 470 475 480

Thr Ile His Asn Phe Cys Asp Ser Val Arg Ala Met Ala Thr Ala Gln
485 490 495

Leu Gly Ser Leu Lys Asn Val Met Leu Val Leu Gly Tyr Lys Arg Lys
500 505 510

Ser Thr Glu Gly Ile Gln Glu Gln Lys Glu Ile Gln Ser Cys Leu Ser
515 520 525

Ile Trp Asp Leu Asn Leu Pro His Glu Val Gln Asn Leu Glu Lys His
530 535 540

Ile Glu Val Arg Thr Glu Leu Ala Asp Lys Met Arg Lys Thr Ser Val
545 550 555 560

Glu

<210> 8

<211> 2949

<212> DNA

<213> Homo sapiens

<400> 8

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gaaaaaatca ttttatcgga gcgtaaaaat gtgccaattg aatttcccgt aattgaccgg 180

aaacgattat tacaactagt gagagaaaat cagctgcagt tagatgaaaa tgagcttcct 240

cacgcagttc actttctaaa tgaatcagga gtccttcttc attttcaaga cccagcactg 300

cagttaagtg acttgtactt tgtggaaccc aagtggcttt gtaaaatcat ggcacagatt 360

ttgacagtga aagtggaagg ttgtccaaaa caccctaagg gcattatttc gcgtagagat 420

gtggaaaaat ttctttcaaa aaaaaggaaa tttccaaaga actacatgtc acagtatttt 480

aagctcctag aaaaattcca gattgctttg ccaataggag aagaatattt gctggttcca 540

agcagtttgt ctgaccacag gcctgtgata gagcttcccc attgtgagaa ctctgaaatt 600

atcatccgac tatatgaaat gccttatttt ccaatgggat tttggtcaag attaatcaat 660

cgattacttg agatttcacc ttacatgctt tcagggagag gctgtattct tttgggccaa 720

gttgtggacc acattgattc tctcatggaa gaatggtttc ctgggttgct ggagattgat 780

atttgtggtg aaggagaaac tctgttgaag aaatgggcat tatatagttt taatgatggt 840

gaagaacatc aaaaaatctt acttgatgac ttgatgaaga aagcagagga agactgtttt 900

gtgtgtattc acttatatcc atcaagtgac tacatttcaa ggcactatat gagaaccata 960

aatattgtac aaacaggatt tgctaaatgt cggtggagag taacagtcca cggggctgat 1020

catggtgatg gcagttttgg atcagtttac cgagcagcct atgaaggaga agaagtggct 1080

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gcaagcattt ggctgggctg tgggcacacc gacagaggac agctctcatt tcttgactta 1920

aatactgaag gatacacttc tgaggaagtt gctgatagta gaatattgtg cttagccttg 1980

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ctggtcatca ataccgaaga tgggaaaaag agacataccc tagaaaagat gactgattct 2100

gtcacttgtt tgtattgcaa ttccttttcc aagcaaagca aacaaaaaaa ttttcttttg 2160

gttggaaccg ctgatggcaa gttagcaatt tttgaagata agactgttaa gcttaaagga 2220

gctgctcctt tgaagatact aaatatagga aatgtcagta ctccattgat gtgtttgagt 2280

gaatccacaa attcaacgga aagaaatgta atgtggggag gatgtggcac aaagattttc 2340

tccttttcta atgatttcac cattcagaaa ctcattgaga caagaacaag ccaactgttt 2400

tcttatgcag ctttcagtga ttccaacatc ataacagtgg tggtagacac tgctctctat 2460

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aagcagaaag agatacaatc ttgcttgacc gtttgggaca tcaatcttcc acatgaagtg 2880

caaaatttag aaaaacacat tgaagtgaga aaagaattag ctgaaaaaat gagacgaaca 2940

tctgttgag 2949

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<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> random primer

<400> 9
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